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TITLE: MATERIALS AND METHODS FOR
IMMUNOCONTRACEPTION

5 **CROSS REFERENCE TO RELATED APPLICATION**

This application is a continuation-in-part of U.S. Application Serial No. 08/012,990, filed January 29, 1993, which is a continuation-in-part of U.S. Application Serial No. 07/973,341, filed on November 9, 1992.

FIELD OF THE INVENTION

10 This invention relates generally to the production and use of zona pellucida proteins, and more particularly to novel DNA sequences encoding zona pellucida proteins, to recombinant materials and methods for producing such proteins and to materials and methods for selectively effecting either transient infertility or permanent sterility in mammals through use of
15 naturally occurring and recombinant zona pellucida proteins.

BACKGROUND OF THE INVENTION

The present invention relates to a method for inducing reproducible transient infertility or sterility in a mammal by inducing in that mammal antibodies directed to proteins found in the zona pellucida of that
20 mammal's oocytes. The invention also relates to purified, isolated DNA sequences encoding the zona pellucida proteins herein designated "ZPA" and "ZPB" and "ZPC" from various mammalian species. The invention is further directed to pharmaceutical compositions capable of inducing antibody production in a subject mammal.

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The zona pellucida (ZP) is a complex matrix surrounding the mammalian oocyte, formed of glycoproteins secreted by ovarian cells. Zona pellucida glycoproteins perform a variety of functions. For example, the mouse ZP proteins previously designated ZP2 and ZP3 are complexed into long filaments which are cross-linked by the protein designated ZP1 in the ZP matrix providing structural integrity to the matrix. Wassarman, P.M., *Annu. Rev. Biochem.* 57:415-442 (1988). In addition to its structural role, mouse ZP3 has been shown to be a sperm receptor in the ZP matrix. Bleil, J.P. and Wassarman, P.M., *Cell* 20: 873-882 (1980). Following binding of sperm to ZP3 and the subsequent induction of the sperm acrosome reaction on the surface of the ZP, ZP2 acts as a secondary sperm receptor that is necessary for the maintenance of sperm binding to the egg. Bleil *et al.*, *Dev. Biol.* 128: 376-385 (1988). Because of its role in the maintenance of the oocyte and in sperm-oocyte interactions, the ZP represents a logical target for design of contraceptive agents which interfere with the fertilization process.

Various groups have undertaken an immunological approach in attempts to interfere with ZP functions and thus to decrease fertility in immunized animals. See, Dunbar *et al.* In: *International Congress on Reproductive Immunology*. T. Wegman and T. Gills (eds.). London: Oxford Press, pp. 505-528 (1983); and Dunbar *et al.* In: *Mechanisms and Control of Animal Fertilization*. J. Hartman (ed.) Academic Press, New York, pp. 139-166 (1983). These studies showed that active immunization of mammals with ovarian homogenates decreased fertility. However, the large number of components in such homogenates made the identification of antigens responsible for the decrease in fertility nearly impossible. In addition, the use of such a complex mixture creates a potential for unwanted and potentially harmful side-effects.

Research by various investigators using chromatographic methods including SDS polyacrylamide gel electrophoresis (PAGE) and high pressure liquid chromatography (HPLC) have resulted in the identification of

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numerous zona pellucida proteins from a variety of mammalian species. Data compiled by Timmons and Dunbar in *"Perspectives in Immunoreproduction: Conception and Contraception"*; pp. 242-260, Mathur, S. and Fredericks, C.M. eds.; New York, Hemisphere Publishing Co (1988), as described below, illustrate examples of zona pellucida proteins that have been characterized.

Zona pellucida proteins isolated from pig include: PZI, a 40-110 kD protein isolated by Dunbar *et al.*, *Biol. Reprod.* 24:1111 (1981); PZII, a 70-110 kD protein, PZIII, a 95-118 kD protein, and PZIV, an 18-25 kD protein, all isolated by Dunbar *et al.*, *Biol. Reprod.* 32:619 (1985); 90K, a 89-119 kD protein, 65K, a 61-83 kD protein, 55K, a 47-66 kD protein, and 25K, an 18-26 kD protein, all isolated by Hedrick, J.L. and Wardrip, N.J. *Biochem.* 157: 63 (1986); ZP1, an 82-118 kD protein, ZP2, a 58-96 kD protein, ZP3 (PPZA), a 40-74 kD protein, and ZP4, a 21 kD protein, all isolated by Subramanian *et al.*, *Biol. Reprod.* 24:933 (1981); 87K (ZP1/ZP2), a 77-97 kD protein, 58K, a 40-70 kD protein both isolated by Yurewicz *et al.*, *Biol. Reprod.* 29: 511 (1983); deglycosylated PZI, a 35 kD protein; PZII, a 55 kD protein; and PZIII, an 80 kD protein all isolated by Skinner and Dunbar as described in *Immunological Approaches to Contraception and the Promotion of Fertility*, G. P. Talwar (ed.) New York: Plenum pp. 251-268 (1986); and deglycosylated ZP3 having a molecular weight of 45 kD isolated by Sacco *et al.*, *J. Reprod. Fertil.* 76:575 (1986).

Isolated rabbit zona pellucida proteins include: RZI, RZII, and RZIII, having molecular weights of 68-125 kD, 80-100.5 kD, and 100-132 kD respectively, all isolated by Dunbar *et al.*, *Biol. Reprod.* 24:1111 (1986); ZP1, ZP2, and ZP3 having molecular weights of 100-118 kD, 83-110 kD, and 80-92 kD respectively, all isolated by Sacco *et al.*, *Proc. Soc. Exp. Biol. Med.* 167:318 (1981); deglycosylated RZI, and RZII having molecular weights of 65 kD, and 80kD respectively, both isolated by Skinner and Dunbar and described in *Immunological Approaches to Contraception and Promotion of Fertility*. G.P. Talwar (ed.). New York: Plenum, pp. 251-268 (1986); and

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deglycosylated RZIII, a 90 kD protein isolated by Timmons and Dunbar, *Biol. Reprod.* 36: 1275 (1987).

A number of mouse zona pellucida proteins have been isolated including: ZP1, ZP2, and ZP3 having molecular weights of 200 kD, 120 kD, and 83 kD respectively, all isolated by Bleil and Wassarman *Dev. Biol.* 76:185 (1980); and ZP1 and ZP2 having molecular weights of 166-122 kD and 90-92 kD respectively, isolated by Sacco *et al.*, *Proc. Soc. Exp. Biol. Med.* 167: 318 (1981). The differences in the molecular weights of mouse ZP1 and ZP2 as reported by Bleil *et al.* and Sacco *et al.* may be due to the fact that Bleil used 2D-PAGE under non-reducing conditions while Sacco used 2D-PAGE under reducing conditions.

The cat zona pellucida proteins CZI and CZII were isolated by Maresh and Dunbar *J. Exp. Zool.* 244:299 (1987) and have molecular weights of 50-110 kD and 90-110 kD respectively.

Maresh and Dunbar *J. Exp. Zool.* 244:299 (1987), have also isolated the dog zona pellucida proteins DZI, DZII, and DZIII which have molecular weights of 50-110 kD, 70-95 kD, and 90-100 kD respectively.

Sacco *et al.*, *Proc. Soc. Exp. Biol. Med.* 167:318 (1981) described squirrel monkey ZP1, ZP2, ZP3, and ZP4 having molecular weights of 63-78 kD, 63-70 kD, 47-51 kD, and 43-47 kD respectively. In the same publication

Sacco *et al.* described human ZP1, ZP2, and ZP3 having molecular weights of 80-120 kD, 73 kD, and 59-65 kD respectively.

To date, few mammalian zona pellucida genes or proteins have been isolated and sequenced. None has been successfully used to produce an effective immunocontraceptive. A lack of consensus among those of skill in the art regarding the number and characteristics (e.g. molecular weight) of proteins present in the zona pellucida of various mammalian species, and difficulties in purifying these heavily glycosylated proteins have hampered

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attempts to utilize zona pellucida proteins to produce an effective immunocontraceptive with predictable function.

A number of groups have had success in cloning cDNAs or genes encoding various mammalian zona pellucida proteins.

- 5 Ringuette *et al.*, *Dev. Biol.*, 127:287-295 (1988) and Liang *et al.*, *Mol. Cell. Biol.*, 10:1507-1515 (1990), reported cloning of mouse DNA encoding zona pellucida proteins ZP3 and ZP2, respectively. The clones were obtained by screening mouse cDNA libraries with anti-ZP3 and anti-ZP2 antibodies. No sequence homology was found between mouse ZP3 and ZP2.
- 10 Ringuette *et al.*, *Proc. Natl. Acad. Sci. USA*, 83:4341-4345 (1986), reported isolation of a partial cDNA clone for mouse ZP3, which clone hybridized with total genomic DNA of mouse, rat, dog, cow, and human, but not with pig or rabbit genomic DNA unless the hybridization was performed at very low stringency. The full length ZP3 cDNA characterized
- 15 by Ringuette *Dev. Biol.* 127:287-295(1988) represents a germ-line specific mRNA having relatively short 5' and 3' untranslated regions and an open reading frame of about 1317 nucleotides with an additional 200-300 nucleotide poly-A tail. Ringuette also found that rat, rabbit, dog, and cow ovary transcribes mRNA which hybridized to the mouse ZP3 cDNA and that the
- 20 ZP3 transcripts had similar molecular weights. Liang *et al. Mol. Cell. Biol.*, 10:1507-1515 (1990), showed that the nucleic acid and deduced amino acid sequence of ZP2 is distinctly different from that of ZP3 although it had the same short motif of 5' and 3' untranslated regions. The ZP2 mRNA is reported to have single open reading frame of 2,139 nucleotides which codes
- 25 for a polypeptide of 80,217 Daltons representing 713 amino acids.

Chamberlin and Dean, *Dev. Biol.* 131:207-214 (1989) and Kinloch, R.A. *et al.*, *Proc. Nat. Acad. Sci. USA*, 85:6409-6413 (1988) have reported the cloning of the mouse ZP3 gene. The mouse ZP3 gene is reported to have 8 exons and 7 introns in a transcription unit of 8.6 kbp.

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Kinloch *et al.*, *Dev. Biol.* 142:414-421 (1990), reported cloning of hamster genomic ZP3 DNA from a hamster genomic DNA library screened with mouse ZP3 DNA as a probe. The hamster ZP3 gene has a transcription unit of 7900 nucleotides and was found to contain 7 introns and 8 exons. The hamster ZP3 protein is approximately 81 % homologous to mouse ZP3 protein. The hamster transcript contained 1266 nucleotides, six less than mouse ZP3 mRNA.

Chamberlain and Dean, *Proc. Natl. Acad. Sci. USA* 87:6014-6018 (1990), reported the cloning of human ZP3 from a human genomic DNA library using mouse ZP3 cDNA as a probe. The human ZP3 gene is composed of 8 exons in a transcription unit of 18.3 kbp. The exons are almost identical in size to the eight exons of mouse ZP3 and the nucleotide sequence of the coding region is 74 % homologous. The human ZP3 transcript is very similar to mouse ZP3 mRNA. Both have short 5' and 3' untranslated regions, and both have a single open reading frame of 1272 nucleotides that encodes a 424-amino acid protein.

U.S. Patent No. 4,996,297, to Dunbar, reported the isolation of three rabbit zona pellucida clones encoding rabbit ZP1 and ZP2 proteins, using anti-ZP1 and anti-ZP2 antibodies as screening probes. The sequences designated as P2 and P3 in Figure 4 of the Dunbar patent represent rabbit ZP cDNAs of 812 and 1705 nucleotides respectively.

Schwoebel *et al.*, *J. Biol. Chem.* 266:7214-7219 (1991), isolated and characterized a full length cDNA (designated rc 55) encoding the 55-kD rabbit zona pellucida protein using cross-species affinity purified antisera. The protein encoded by this cDNA has some similarity to the mouse ZP2 protein described by Liang. However, comparisons of rc 55 with the mouse ZP3 protein revealed no homology.

The functional activities of the cloned ZP DNAs and their encoded proteins have not been fully characterized and neither has their potential use as immunocontraceptives been demonstrated.

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In order to develop a useful zona pellucida product for use in fertility control, particularly in the form of a vaccine, it is highly desirable to purify, isolate, and characterize zona pellucida proteins from a species of an animal of interest. Because of factors such as the purity of such proteins
5 needed for vaccine production, and the high cost and numerous problems associated with purification of these proteins, it would be highly desirable to ascertain the DNA and amino acid sequences of zona pellucida proteins of a specific species of interest. Having such known, isolated and characterized zona pellucida proteins, the function of each zona pellucida protein may be
10 understood and a fertility control product may be designed based upon the specific functional characteristics of a particular zona pellucida protein and for a particular mammalian species.

It would be thus highly useful and desirable to provide isolated, purified, sequenced, and characterized recombinant zona pellucida proteins
15 which would permit the development of fertility control products possessing specific reproducible effects in eliciting transient and/or permanent infertility. Such products, where used to elicit transient infertility, would desirably have long lasting effects so as to minimize the number of times the immunocontraceptive agent must be administered to maintain infertility.

20 SUMMARY OF THE INVENTION

The present invention provides novel methods and materials for inducing either reproducible transient or permanent infertility effects in female mammals, including humans, by selective administration of homologous and/or heterologous mammalian species ZP proteins or immunocontraceptively
25 active fragments thereof hereinafter designated as ZPA, ZPB and ZPC. By "reproducible" is meant that, unlike prior art attempts to induce transient infertility by administration of ZP proteins (in the form of mixtures of such proteins), this invention achieves its transient infertility effects by the administration of ZPA and/or ZPB in a form such that the duration of

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transient infertility is controllable and can be maintained in an on or off condition in a controllable and/or predictable fashion. This is achieved primarily through administration of the highly pure ZPA and ZPB proteins or immunocontraceptively active fragments thereof of this invention, e.g., in
5 recombinant form and thus essentially devoid of ZPC. By immunocontraceptively active fragments is meant a ZP protein fragment capable of inducing infertility.

In one of its aspects, the present invention provides methods for inducing reproducible transient infertility in a mammal by administering to a
10 subject female mammal a zona pellucida protein (or fragment thereof) selected from the group consisting of mammalian ZPA, and ZPB, and combinations thereof in doses effective to stimulate production in said mammal of antibodies which recognize ZPA or ZPB proteins of said mammal. It is presently preferred that mammalian ZPA and ZPB for use in such methods be derived
15 from the same mammalian species as the subject mammal although the use of heterologous species proteins is also contemplated. Use of purified isolates of mammalian ZPA or ZPB protein such as obtained by chromatographic separatory procedures is contemplated. Use of proteins produced by recombinant methods is expected to be most preferred.

20 According to another aspect of the invention, methods are provided for inducing permanent sterility in a female mammal by administering to a subject female mammal a recombinant mammalian ZPC protein (or fragment thereof) in a form essentially devoid of ZPA and/or ZPB, in a dose effective to stimulate production in said female mammal of
25 antibodies which recognize the ZPC protein of said mammal. As is the case with induction of transient infertility, use of homologous species ZPC is preferred, but not required, and the protein may be derived from natural sources or produced by recombinant methods. Modified ZPC proteins including but not limited to palmitylated and chitosan modified proteins are
30 also contemplated by the present invention.

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Presently preferred ZPA, ZPB, and ZPC proteins for veterinary application of the transient infertility and sterility inducing methods include porcine, rabbit, canine, feline, bovine, and cynomolgus monkey ZP proteins.

In another of its aspects, the present invention provides
5 pharmaceutical compositions for use in inducing reproducible transient infertility in a female mammal (including humans) comprising an effective dose of a zona pellucida protein (or fragment thereof) selected from the group consisting of mammalian ZPA, and ZPB (substantially free of ZPC), in combination with one or more pharmaceutically acceptable carriers, diluents
10 and adjuvants. Modified ZPA and ZPB proteins (for example, palmitylated or chitosan modified) are also contemplated by the present invention.

According to another aspect of the present invention, novel purified and isolated DNA sequences are provided which encode porcine ZPA, ZPB, and ZPC, as illustrated by the DNA sequences set out in SEQ ID NOS.
15 1, 3, and 5. Also, provided are purified and isolated DNA sequences encoding: rabbit ZPC, as illustrated by the DNA sequence set out in SEQ ID NO. 7; canine ZPA and ZPC, as illustrated by the DNA sequences set out in SEQ ID NOS. 9 and 11; feline ZPA, ZPB, and ZPC, as illustrated by the DNA sequences set out in SEQ ID NOS. 13, 15, and 17; bovine ZPA, ZPB,
20 and ZPC, as illustrated by the DNA sequences set out in SEQ ID NOS. 19, 21, and 23; human ZPA and ZPB as illustrated by sequences set out in SEQ ID NO. 42 and 40, respectively, and as contained as human DNA inserts in lambda phage clones A1 and A4, (ZPA) and as contained in human DNA inserts in lambda phage clones 1-1 and 4-9 (ZPB).

25 Polynucleotide sequences of the invention are useful for the production of ZPA, ZPB and ZPC proteins by recombinant methods and as probes for the isolation of heterologous species polynucleotides encoding corresponding zona pellucida proteins by hybridization methods.

Also provided by the present invention are novel host cells,
30 especially unicellular eucaryotic and procaryotic cells, stably transformed or

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transfected with polynucleotides of the invention in a manner allowing expression of the ZP proteins (or immunologically significant fragments thereof) in the host cells. Host cells expressing such ZP products, when grown in a suitable culture medium, and particularly useful for large scale
5 production processes wherein the desired polypeptide products, in glycosylated or non-glycosylated form are isolated from the cells or the medium in which the cells are grown.

Recombinant polypeptides provided by the invention thus comprise ZPA, ZPB and ZPC, and full equivalents of such zona pellucida
10 proteins including both glycosylated and non-glycosylated forms, variants and immunologically active fragments thereof which retain substantial biological activity, i.e., at least one of the biological activities of the zona pellucida protein discussed herein, e.g., the ability to stimulate the production of antibodies as discussed herein upon administration to a mammal. Such
15 immunologically active fragments may be defined as containing at least one epitope effective to stimulate the production of antibodies upon administration to a mammal in accordance with this invention.

In another aspect of the invention, a method is provided for the isolation of nucleic acid sequences encoding other mammalian ZPA, ZPB, and
20 ZPC proteins by hybridization under stringent conditions of heterologous species ZPA, ZPB, and/or ZPC probes to cDNA or genomic DNA libraries, derived from the mammalian species of interest.

More particularly, it is an aspect of the invention to provide a method for the isolation of nucleic acid sequences encoding human ZPA and
25 ZPB by hybridization under stringent conditions of sequences encoding ZPA and/or ZPB from heterologous species.

Other aspects and advantages of the present invention will be readily understood upon consideration of the following detailed description of presently preferred embodiments thereof, reference being made to the figures
30 wherein:

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DESCRIPTION OF THE FIGURES

Fig. 1 is a diagrammatic representation of the plasmid vector pZ90;

Fig. 2 is a diagrammatic representation of the plasmid vector pZ98; and

Fig. 3 is a diagrammatic representation of the plasmid vector pZ156.

Fig. 4 is a diagrammatic representation of the alignment of the Eco R1 fragments encoding human ZPB.

Fig. 5 is a diagrammatic representation of the plasmid vector pZ169.

Fig. 6 is a diagrammatic representation of the plasmid vector pZ145.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to mammalian zona pellucida proteins characterized in three major classes: ZPA, ZPB, and ZPC. This classification scheme has resulted from repetitive screening of various mammalian ovarian cDNA libraries and retrieval of clones which encode proteins showing significant homology in three distinct groups, designated herein as ZPA, ZPB and ZPC. Although similarity is seen between DNA sequences encoding ZPA, ZPB, or ZPC between animal species, very little homology is found between the individual species' ZPA, ZPB, and ZPC proteins.

DNA sequences encoding zona pellucida proteins A, B, and C and their deduced amino acid sequences for various mammalian species ZPs are presented in SEQ ID NOS. 1-24. It is understood that the DNA sequence of a particular animal may vary slightly due to the phenomenon of allelic variation. Small differences in the precise DNA sequence between animals or slight errors due to the inefficiency of sequencing procedures are to be

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expected. Such variants are included within the scope of the present invention.

The zona pellucida DNA sequences described above were obtained from ovarian cDNA libraries screened with specific zona pellucida antibodies or known zona pellucida DNA probes. Comparison of isolated
5 sequences to published protein or DNA sequences and with other clones as they were isolated was used to classify and identify the clones as described above.

The term "zona pellucida protein" is meant to include full
10 length proteins ZPA, ZPB, and ZPC, as well as expected variants, immunologically active fragments or peptides contained within these proteins. The term "zona pellucida DNA" is meant to include those nucleic acid sequences encoding zona pellucida protein or fragments thereof.

The three major classes of mammalian zona pellucida proteins
15 have been determined on the basis of homology within the DNAs encoding ZP proteins of a variety of mammalian species. ZPA includes those peptides previously, variously described in the literature as ZP1, ZP2, and ZP4; ZPB includes those peptides previously, variously described as ZP3 α and rc 55; and ZPC includes those peptides previously variously described as ZP3 β and
20 ZP3.

The homology of various species of zona pellucida proteins within a specific class as compared with a consensus sequence for each class is shown in Table 1. The consensus sequence was derived using the Microgenie® Sequence Analysis Program (Beckman Instruments, Inc. Spinco
25 Division, Palo Alto, CA). The minimum percent of aligned sequences which must have the same residue at a given position for that residue to be included in the consensus sequence was 50%. The DNA sequences corresponding to the amino acid consensus sequences for ZPA, ZPB, and ZPC proteins are set out in SEQ ID NOS 25, 26, and 27, respectively.

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TABLE 1

HOMOLOGY OF DEDUCED ZP PROTEINS AMINO ACIDS

		<u>ZPA</u>	<u>ZPB</u>	<u>ZPC</u>
	DOG	78.9%	--	77.3%
5	CAT	78.4%	70.9%	77.5%
	COW	77.2%	80.4%	77.2%
	PIG	73.0%	77.8%	79.0%
	RABBIT	70.1%	74.6%	71.3%
	MOUSE	61.6%	--	69.6%
10	HUMAN	--	--	76.9%
	HAMSTER	--	--	70.5%

The deduced amino acid sequences of the various species of zona pellucida proteins suggest approximate unglycosylated molecular weights of 75 kD, 55 kD, and 45 kD for ZPA, ZPB, and ZPC, respectively. A more detailed analysis of both DNA sequence homology and deduced amino acid sequence homology is set out as Examples 13, 14, and 15.

It has surprisingly been found that administration of a specific class of zona pellucida protein to a host animal results in a specific immunocontraceptive effect and that selection of the appropriate ZP protein for administration allows induction of desired contraceptive results, in terms of permanent sterility or transient infertility. For example, vaccination of an animal with zona pellucida protein C induces antibody titers in that animal which recognize endogenous ZPC resulting in loss of oocytes from the animal's ovary, thereby causing permanent sterility. In contrast, vaccination of an animal with zona pellucida protein A, B or combinations thereof induces antibody titers which do not recognize ZPC, but recognize ZPA and/or ZPB. This results in cycling, infertile animals for the time period during which

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anti-ZPA and/or anti-ZPB antibody titers remain high. When such antibody titers fall, the infertility effect is diminished, and the animal regains fertility.

Vaccination with the purified, isolated, and characterized ZPA, ZPB, or ZPC proteins is seen to exert a specific effect on the immunized animal if an autoimmune response is triggered wherein the autoantibodies generated specifically recognize the immunized animals' own specific zona pellucida protein. This self-recognition for antibodies induced according to the present invention may be defined and characterized by the ability of serum antibodies to recognize at least one epitope present on a homologous species zona pellucida protein.

In the preferred method of the invention, an animal is immunized with a recombinant ZPA, ZPB, or ZPC or fragments thereof. The recombinant protein or peptide may be of homologous species or derived from a heterologous species zona pellucida which shares common epitopic determinants, with the proviso that such common epitopic determinants function to induce the desired autoimmune response.

The recombinant protein or peptide fragment may be chemically conjugated to immune enhancing agents such as Keyhole Limpet Hemocyanin (KLH), and Muramyl dipeptide (MDP), and the like, or alternatively may be provided in the form of a fusion protein, e.g., with foreign protein amino acids at the amino and/or carboxy terminus. Fully conventional methods for stimulating the production of antibodies upon administration of the proteins or fragments of this invention are well known; similarly, passive immunization techniques involving administration of antibodies *per se*, e.g., anti-ZPA antibodies, anti-ZPB antibodies, or anti-ZPC antibodies, to the zona pellucida proteins or fragments of this invention is also within the scope of the invention. For details, see Dean, PCT Application WO90/15624 whose disclosure is entirely incorporated by reference herein.

Thus, to induce permanent sterility in a dog, recombinant canine ZPC may be employed which is expressed as a bacterial fusion protein

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(or conjugated to immune enhancing agents) wherein active canine ZPC protein is conserved and available for interaction with antigen presenting cells. The expressed protein is then administered to a host dog and induces an autoimmune response in which generated antibodies recognize canine zona pellucida protein C. This autoimmune effect, which specifically recognizes dog ZPC protein or its aggregates, induces permanent sterility in the vaccinated dog, which sterility is associated with a loss of oocytes from the dog's ovary.

Alternately, a non-homologous species ZPC, such as recombinant porcine ZPC or peptides thereof which are cross-reactive with canine ZPC, can be administered to a dog to achieve similar sterilizing effects. The sterilizing effect, however, is only realized when antibodies capable of recognizing the host's own native zona pellucida are induced (or administered in the context of passive immunization).

In an alternative embodiment of the present invention, the administration of a host species' own A and/or B class zona pellucida protein, or a related A and/or B protein from another species which induce antibodies against the host's ZPA and/or ZPB proteins results in an infertility effect which is distinct from that produced by ZPC class antigens. The physiological effect of vaccination with the ZPA and ZPB proteins is a transient one. "Transient infertility" is herein defined as infertility which is maintained when antibodies against self-zona pellucida proteins are sustained in the host animal's circulation at a contraceptively effective concentration (e.g., at titers of approximately 1:250 in the dog) and which infertility is diminished when antibodies against self fall below a contraceptively effective lower limit. The reduction in antibodies against self-zona pellucida results in restoration of fertility without evidence of major physiological changes in the ovary. Typically, the reduction in antibody titers occur by natural processes in the mammalian host, but other methods of reducing antibody titers are within the scope of the invention.

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Contraceptively effective antibody titers against self zona pellucida proteins A and B required to maintain infertility will vary with the species of vaccinated animal as well as with the species of recombinant ZPA or ZPB peptide administered, but may readily be determined, for example, by testing a panel of the desired animal species with varying doses of the specific antigen, measuring the induced titer of anti-self antibodies by known ELISA techniques, and correlating the titers with reproductive indicators, e.g., cycling, hormone levels, and the like. In general, antibody titers greater than 1:250 are contraceptively effective.

Based on amino acid sequence homologies, it is expected that all zona pellucida proteins of a particular class contain functional epitopes which are cross-reactive between mammalian species. However, absent characterization and identification of such functional cross-reactive epitopes, a preferred, selective contraceptive agent is a homologous species zona pellucida protein or antibody thereto.

The present invention will be more completely understood upon consideration of the following illustrative examples of the practice thereof wherein: Example 1 addresses the isolation of DNAs encoding porcine species ZPA, ZPB and ZPC; Example 2 relates to isolation of rabbit ZPC DNA; Example 3 relates to isolation of DNAs encoding canine ZPA and ZPC; Example 4 addresses isolation of feline DNAs encoding ZPA, ZPB and ZPC; Example 5 relates to cloning and isolation of DNAs encoding bovine species ZPA, ZPB and ZPC; Examples 6 and 7 describe immunocontraceptive treatment of dogs with naturally-derived porcine zona pellucida proteins; Example 8 relates to serochemical studies on animals treated in Examples 6 and 7; and Examples 9 and 10 address recombinant production of a canine ZPC fusion protein and its immunocontraceptive use in dogs. Example 11 relates to the isolation of DNAs encoding human ZPA and ZPB by methods described herein. Example 12 relates to the isolation and sequencing of DNAs encoding cynomolgus monkey ZPA, ZPB and ZPC. Examples 13-15 relate

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to the comparison of the DNA sequence and the deduced amino acid sequence of mammalian ZPA, ZPB, and ZPC, respectively. Example 16 relates to the immunization of cynomolgus monkey using HSPZ and fractionated HZPC. Example 17 relates to the mapping of mammalian zona pellucida protein epitopes. Example 18 describes the immunization of dogs using recombinant ZPC proteins. Example 19 relates to the vaccination of cows and cats with recombinant ZP proteins.

Example 1

Isolation of DNA Sequences Encoding

10 Porcine Zona Pellucida Proteins ZPA, ZPB, and ZPC.

A cDNA library in λ gt11 was commercially prepared by Clone Tech, Palo Alto, CA, from an ovary isolated from a 14 week old pig and was screened using an anti-ZP3 β antibody obtained from E.C. Yurewicz and described in Keenan *et al.*, *Biol. Reprod.*, 44:150-156 (1991). Eight
15 candidate clones were identified.

A degenerate DNA oligonucleotide probe (19bps) was constructed to represent all possible sequences of a short portion of the N-terminus porcine ZP3 β as described in Yurewicz *et al.*, *J. Biol. Chem.*, 262:564-571, (1987). The degenerate probe sequence is set out in SEQ ID
20 NO. 28.

Southern analysis of the eight candidate clones isolated by expression screening with the degenerate DNA oligonucleotide probe resulted in hybridization with two of the eight candidates. The two clones recognized by the degenerate probe were then subcloned into the pBS KS plasmid
25 (STRATAGENE Cloning Systems, La Jolla, CA) for sequence analysis using the sequence enzyme and the protocol described in the SEQUENASE[®] Manual (U.S. Biochemical, Cleveland, OH). One of the clones, B-8, having an insert size of approximately 1200 base pairs, included a sequence homologous to the

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N-terminal sequence of mouse ZP3, previously identified by Ringuette *et al.*, *Dev. Biol.*, 127:287-295, (1988). The remaining clone, B-6, had an insert size of approximately 1000 base pairs. Neither hybridizing clone contained the C-terminal portion of the gene, as suggested by the lack of homology to the mouse ZP3 gene in this region.

The 14-week porcine ovarian library was then rescreened by DNA hybridization. Approximately 150,000 PFUs were plated on agar plates with *E. coli* Y1090. After overnight incubation at 37°C, nylon membrane lifts of plaques were prepared and screened using the B6 and B8 clones derived above isolated by screening with the degenerate oligonucleotide probe set out in SEQ ID NO. 28.

Filters were prehybridized in a solution containing 5X saline, sodium phosphate, EDTA buffer (SSPE), 5X Denhardt's Reagent, 100µg/ml salmon sperm DNA, 30% formamide and 0.5% SDS for three hours at 42°C. Approximately 50 ml of the prehybridization solution was used for 12 filters (132 mm). After prehybridization, 10 ng of freshly radiolabeled DNA probe in 30% formamide, 5X SSPE was added. The probes were heat denatured at 95°C for 3-5 minutes and hybridization with the DNA probes continued overnight at 42°C. The hybridized filters were then washed twice with 100 ml of 5X SSPE at 55°C, for approximately one hour each wash. The filters were then rinsed with 250 ml of 5X SSPE at room temperature and allowed to air dry. The dried filters were exposed to x-ray film at -70°C using intensifier screens for at least eight hours and the films were developed for visual analysis.

Among the additional clones isolated were two clones including the C-terminal portion of the porcine ZP3β gene. One clone, λ5-1, was subcloned into plasmid pBS KS and sequenced. This plasmid, termed pZ57, contained a ZP DNA insert having 1266 base pairs and appeared to encode the full length amino acid sequence of porcine ZP3β as compared with known mouse ZP3. Alignment of the deduced amino acid sequence of the clone with

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the known N-terminal amino acid sequence of ZP3 β reported by Yurewicz *et al.*, *J. Biol. Chem.*, 262:564-571 (1987), and an internal peptide sequence of ZP3 β corresponding to amino acids 255-274 as provided by E.C. Yurewicz confirmed the identity of this clone as encoding porcine ZP3 β .

5 The DNA sequence of this clone, termed porcine ZPC, is set out in SEQ ID NO. 5 and its deduced amino acid sequence is set out in SEQ ID NO. 6.

 The 14-week porcine ovarian cDNA library was further screened using rabbit zona pellucida rc 55 cDNA as a probe [described in
10 Schwoebel *et al.*, *J. Biol. Chem.*, 266:7214-7219, (1991)].

 One candidate clone of approximately 1700 base pairs, λ 2-1, was isolated and was transferred into the sequencing plasmid pBS KS. The DNA sequence and deduced amino acid sequence of the porcine DNA insert was determined using the method described in the SEQUENASE[®] manual (US
15 Biochemical Corporation, Cleveland, Ohio). The sequenced clone contained 1620 base pairs and included a full length copy of the porcine ZP3 α gene as confirmed by alignment of the deduced amino acid sequence with portions of the known protein sequence of porcine ZP3 α provided by E.C. Yurewicz between amino acids 206-222, 271-279, and 328- 344. The DNA sequence
20 of this clone, termed porcine ZPB, is set out in SEQ ID NO. 3. Its deduced amino acid set out in SEQ ID NO. 4.

 The 14-week porcine ovarian library was further screened using the procedure described above and using a DNA probe encoding canine ZPA protein (as obtained in Example 3 below, SEQ ID NO. 9). A single clone,
25 λ 3-5 having approximately 1300 base pairs, was obtained representing the N-terminal 60% of the theoretical porcine ZPA gene as estimated by the size of the clone in relation to the ZP2 gene isolated from mouse by Liang *et al.*, *Mol. Cell. Biol.* 10:1507-1515 (1990), and rabbit by Dunbar, U.S. Patent No. 4,996,297, and dog (see Example 3 below).

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This clone was then used to rescreen the porcine ovarian library. Three additional clones were obtained, two small clones and one clone large enough to contain the full length sequence. The large candidate clone, λ B, having approximately 2200 base pairs, was sequenced, and the data
5 showed this ZPA clone to lack only approximately seven base pairs of the full length sequence including the ATG start codon when aligned with the mouse ZP2 gene and the canine ZPA gene described in Example 3. The DNA sequence of this clone, termed porcine ZPA, is set out in SEQ ID NO. 1. Its deduced amino acid sequence is set out in SEQ ID NO. 2.

10 This isolated porcine clone included sequences corresponding to published sequences of three identified porcine zona pellucida proteins, ZP1 (80kD), ZP2 (62kD) as disclosed in U.S. Patent No. 4,996,297 to Dunbar and ZP4 (21kD) as disclosed by Hasegawa *et al.*, Abst. No. 382, *Meeting Soc. Study Reprod.* July, 1991. These results suggest that a singular clone encodes
15 one zona pellucida protein which previously had been thought to exist as three separate proteins, i.e., ZP1, ZP2, and ZP4. This further suggests that only three major porcine zona pellucida genes encode three major zona pellucida proteins which here are termed ZPA, ZPB, and ZPC. ZPA includes those proteins previously identified as ZP1, ZP2, and ZP4. ZPB corresponds to
20 ZP3 α and ZPC corresponds to previously identified ZP3 β . Yurewicz *et al.* *J. Biol. Chem.*, 262:564-571, (1987).

Example 2

Isolation and Purification of DNA Sequences

Encoding Rabbit ZPC Protein

25 Ovaries were removed from five week old rabbits and mRNA was prepared using the Fast Track™ mRNA isolation kit in accordance with the procedure described in the *Fast Track™* instruction manual, version 3.1, catalog No. K1593-02 (Invitrogen, San Diego, CA). A Lambda Librarian™

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kit (Invitrogen, San Diego, CA) was used to prepare cDNA and to clone cDNAs into λ gt10 according to the manufacturer's instructions. Approximately 150,000 PFUs were plated on agar plates with *E. coli* Y1090. After overnight incubation at 37°C, nylon membrane lifts of colonies were prepared and screened with a porcine ZPC DNA probe using the screening procedures described for Example 1. The probe used was the porcine ZPC sequence as set out in SEQ ID NO. 5.

Two positive clones, λ R4 and λ R5, hybridized with the porcine ZPC DNA. The size of each of these clones as estimated in agarose gels was approximately 1300 base pairs. Both λ R4 and λ R5 were sequenced as described for Example 1. The sequences were identical except that λ R5 contained four additional nucleotides at the 5' end. The determined DNA sequence was approximately 75% homologous to the DNA sequence encoding porcine ZPC.

The DNA sequence encoding rabbit ZPC protein is set out in SEQ ID NO. 7. Its deduced amino acid sequence is set out in SEQ ID NO. 8.

Rabbit ZPA and ZPB proteins have been previously identified by Dunbar in U.S. Patent No. 4,996,297 as P2 and P3, respectively.

20

Example 3

Isolation of DNA Sequences Encoding Canine Zona Pellucida Proteins ZPA and ZPC

A 16 week canine ovarian cDNA expression library was commercially prepared by Clone Tech, Palo Alto, CA, in λ gt11 generally following the methods described in Example 1. The canine ovarian cDNA library was screened using antibodies raised against heat solubilized canine zona pellucida. Heat solubilized canine zona pellucida (HSDZ) was prepared generally following the procedures described in Dunbar *et al. Biochemistry*,

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19:356-365, (1980) except ganged razor blades were used to mince the ovaries.

Rabbits were immunized with 250 μ g HSDZ and 250 μ g MDP.

Two additional boosts followed at approximately three week intervals. The
5 resultant rabbit serum was used to screen the canine ovarian cDNA expression
library. Seven candidate clones were obtained. Cross-hybridization
experiments were performed by Southern blot analysis as follows. The largest
clone, λ 26-1, having approximately 1300 base pairs, was first used as a probe
against all of the other clones in Southern blots. Three other clones were
10 identified. The largest of the remaining clones, λ 20-1 and λ 7-1, having
approximately 800 and 1000 base pairs respectively, were then used as probes
in Southern blots. These probes identified no additional clones. This cross
hybridization analysis of the seven candidate clones to each other indicated
that four of these clones were related, e.g. four clones hybridized to λ 26-1
15 while the remaining three λ 20-1, λ 7-1, and λ 19-3 were independent.

The largest of the four related clones, λ 26-1, was subcloned
into pBS KS plasmid for sequence analysis according to the procedure
described in Example 1. The analyzed sequence demonstrated the presence
of a long open reading frame of 1278 base pairs encoding a protein of
20 approximately 426 amino acids. Comparison of the deduced amino acid
sequence of this clone with the sequences of known zona pellucida proteins,
indicated this clone encoded a protein related to mouse ZP3 (ZPC) as reported
by Ringuelette *et al.*, *Dev. Biol.* 127:287-295 (1988), hamster ZP3 as reported
by Kinloch *et al.*, *Dev. Biol.*, 142:414-421 (1990), human ZP3 as reported by
25 Chamberlin *et al.*, *Proc. Natl. Acad. Sci. USA* 87:6014- 6018 (1990) and
porcine ZPC protein (see Example 1). The DNA sequence of this clone,
termed canine ZPC, is set out in SEQ ID NO. 11. Its deduced amino acid
sequence is set out in SEQ ID NO. 12.

The remaining three independent candidate clones were
30 subcloned into the pBS KS plasmid for sequence analysis as described above.

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The determined sequence of the 800 base pair clone, λ 20-1, was compared with known ZP sequences by computer analysis as described above and was found to be related to the mouse ZP2 (ZPA) [Liang *et al.*, *Mol. Cell. Biol.* 10:1507-1515 (1990)] and porcine ZPA (see Example 1).

5 The 800 base pair fragment from λ 20-1, was then used as a hybridization probe to rescreen the canine cDNA library. Two additional candidate clones were identified, the larger of which, λ 7A, having approximately 2800 base pairs, was subcloned into pBS KS plasmid for sequence analysis. Comparison of this sequence with known sequences
10 encoding zona pellucida proteins suggested the candidate clone λ 7A contained a full length ZPA sequence, but an incorrect N-terminal sequence, e.g., the clone contained an additional 600 base pairs as determined by alignment with known mouse ZP2 and rabbit ZPA sequences referenced in Example 1. The second candidate clone, λ 9-2, having approximately 1000 base pairs, was then
15 subcloned into the plasmid pBS KS and sequenced. The sequence of the second clone indicated the presence of a correct N-terminal sequence, but included only approximately the N-terminal 40% of the full length clone as determined by alignment with the mouse ZP2 and rabbit ZPA genes. Overlap of the two cDNA clones, however, provided the full length sequence.

20 The appropriate pieces of each clone were subcloned as follows to generate the correct full length zona pellucida clone containing a 2028 base pair open reading frame encoding a protein of approximately 676 amino acids. The λ 7A DNA was digested with Eco RI to yield two insert fragments (2000 bps and 800 bps). These two fragments were each subcloned into pBS KS
25 yielding pZ36 and pZ37, respectively. Plasmid pZ37 carried the C-terminal portion of this sequence. The λ 9-2 DNA insert was removed from the λ vector and subcloned into pBS KS to yield pZ38. Plasmid pZ36 was digested with Hind III to remove approximately 1350 bps of the N-terminal portion of the λ 7A gene fragment (about 850 bps of nonsense DNA and 500 bps of
30 coding sequence). This digestion also removed one of the Eco RI insert ends

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and left a single Eco RI site. The pZ37 Eco RI insert was then moved into the single remaining Eco RI site in the modified pZ36 (pZ36 Δ 1) to reestablish the relative DNA structure orientation that existed in the λ 7A insert (1450/2800 bps). This combined plasmid was then opened with Hind III and the Hind III fragment from pZ38 carrying the N-terminal ZP DNA sequence was inserted to create plasmid pZ39 which is a pBS KS carrying the full length canine ZPA sequence. The DNA sequence of this canine ZPA gene is set out in SEQ ID NO. 9. Its deduced amino acid sequence set out in SEQ ID NO. 10.

10

Example 4

Isolation of DNA Sequences Encoding Feline Zona Pellucida Proteins ZPA, ZPB, and ZPC

Ovaries were isolated from five cats approximately three to four months in age. Messenger RNA was isolated from six ovaries using the Fast Track™ mRNA Isolation Kit (Invitrogen, San Diego, CA, Catalog No. K1593-02) using the protocol provided with the kit. cDNA was prepared using the protocol and cloned into λ gt10 as described in Example 2.

Approximately 150,000 plaque forming units (PFUs) were plated on agar plates with *E. coli* Y1090. After overnight incubation at 37°C, nylon transfer membranes were used to prepare and screen plaque lifts. Plaques were screened using a mixture of DNA probes in equal proportions encoding porcine ZPA, ZPB, and ZPC proteins and using the hybridization procedure as described for Example 2. A total of 81 positive clones were identified. Twelve of these clones were plaque-purified. Southern analysis of these clones using porcine ZPA, ZPB, and ZPC DNAs individually as probes indicated that seven of these clones encoded ZPC proteins and one clone encoded a ZPA protein. Four of the clones contained inserts which could not be separated by Eco RI digestion

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Five of the ZPC clones were between 1200-1350 base pairs in length. One clone, λ C-112, having approximately 1350 base pairs was subjected to sequence analysis as described above and its deduced amino acid sequence was found to be approximately 70% homologous to the canine ZPC protein obtained in Example 3. The DNA sequence of this feline ZPC clone is set out in SEQ ID NO. 17. Its deduced amino acid sequence is set out in SEQ ID NO. 18.

The single feline ZPA clone, λ C-116, was sequenced and found to be approximately 2215 base pairs in length. The deduced amino acid sequence was approximately 75% homologous to the canine ZPA protein characterized in Example 5. The DNA sequence of this feline ZPA clone is set out in SEQ ID NO. 13. Its deduced amino acid sequence is set out in SEQ ID NO. 14.

The remaining 69 positive clones were rescreened using porcine ZPB DNA as a probe (SEQ ID NO. 3). Ten positive clones were obtained. The largest clone, λ C-1, contained approximately 1.7 kilobases as determined by agarose gel electrophoresis. This clone was sequenced, and its deduced amino acid sequence was found to be approximately 80% homologous to the porcine ZPB protein described in Example 1. The DNA sequence of this feline ZPB clone is set out in SEQ ID NO. 15. Its deduced amino acid sequence is set out in SEQ ID NO. 16.

Example 5

Isolation of DNA Sequences Encoding Bovine Zona

Pellucida-Proteins ZPA, ZPB, and ZPC

A cDNA library was constructed from a five month bovine ovary by the method described in Example 2. The bovine ovarian library was screened with DNA hybridization probes representing each of the classes of zona pellucida proteins using a mixture of equal proportions of porcine

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DNA probes encoding ZPA (SEQ ID NO. 1), ZPB (SEQ ID NO. 3), and ZPC (SEQ ID NO. 5) proteins, as described for Example 2 and using the procedures described for Example 1. Initial screening yielded three candidate clones. Southern analysis of these clones with individual porcine ZPA, ZPB, and ZPC DNA probes used in the initial screening indicated that one of the clones, λ B2, having approximately 650 base pairs, encoded ZPA. A second clone, λ B-1 having approximately 1000 base pairs encoded ZPB. A third clone, λ B14, having approximately 1200 base pairs, encoded ZPC.

The bovine ovarian library was then rescreened with the mixed porcine ZP DNA probes. Two additional clones were obtained and identified by Southern analysis as encoding ZPC.

The Eco RI inserts of the ZPA, ZPB, and largest ZPC clone were subcloned and their DNA sequences analyzed. The sequences encoding these bovine ZPA, ZPB and ZPC fragments were set out in SEQ ID NOS. 19, 21, and 23, respectively. Their deduced amino acid sequences are set out in SEQ ID NOS. 20, 22, and 24, respectively.

Example 6

Immunization of Dogs with Heat-Solubilized Fractionated Porcine Zona Pellucida

Heat-solubilized, porcine zona pellucida (HSPZ) was prepared generally following the procedures described by Dunbar *et al. Biochemistry*, 19:356-365, (1980) but using a hand powered meat grinder instead of the Zonamatic described. Following isolation, the zona pellucida protein was solubilized in 0.1 M sodium carbonate buffer, pH 9.6, and was dialyzed extensively against 6M urea. The resultant solution, a volume of 2-3ml containing approximately 12 μ g of HSPZ, was subjected to isoelectric-focusing in a BIORAD Rotofor isoelectric-focusing chamber as follows. An isoelectric gradient was established using 1% ampholytes having a pI range of 3-10. The

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zona pellucida protein was introduced into the mid-range chamber (pI 7.0) and allowed to focus for approximately four hours at 4°C or until the voltage stabilized.

Twenty isoelectrically focused fractions were collected and
 5 analyzed by SDS PAGE and Western blot analysis for pig zona pellucida proteins. Acidic fractions having a pI range of approximately 3.5-5.5 and which contained the porcine zona pellucida proteins were combined. The fractions were dialyzed into 0.1M carbonate buffer, pH 9.6 and concentrated to approximately 3mg/ml. This antigenic preparation was used to vaccinate
 10 animals as described below. Analysis of this antigenic preparation by two-dimensional gel electrophoresis indicated the presence of ZPA and ZPB protein. However, ZPC was not revealed to be present in this preparation.

The HSPZ antigenic preparation was added to a 50/50 water oil emulsion with incomplete Freund's adjuvant (Sigma, St. Louis, MO)
 15 containing 250µg of MDP per dose. One ml of the 50/50 water oil emulsion contained 0.425 ml paraffin oil, 0.075 ml mannide monooleate, and 0.5 ml PBS containing 250 µg threonyl-MDP (SYNTEX Corporation) and the amount of HSPZ described in Table 3 below.

Four random breed dogs aged 10-12 weeks were immunized
 20 with HSPZ using the regimen described in Table 2.

TABLE 2

			<u>mg HSPZ</u>
	Prime	Time 0	0.1
	Boost #1	Week 4	1.0
25	Boost #2	Week 8	0.25
	Boost #3	Week 12	0.2
	Boost #4	Week 16	1.0
	Boost #5	Week 36	1.0

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The antisera produced by these animals was monitored via ELISA methodology. By week 17 antibody titers against self, e.g. against canine zona pellucida proteins, had reached a maximum (8-16K by ELISA) and thereafter began to drop.

5 At week 36, one animal was unilaterally ovariectomized and the removed ovary was sectioned and stained with periodic acid schiff stain (PAS) for histological examination. The ovary appeared normal, as evidenced by the presence of follicles in all stages of development. At week 52, two of the
10 four test animals were observed to exhibit estrus behavior. The remaining two test animals exhibited estrus behavior at approximately one and a half years when the first two test animals experienced their second heat. All test animals were bred repeatedly with competent males and by artificial insemination, however, none became pregnant. During this same period,
15 animals in various test regimens in which no self titers were obtained, as described in Example 10, became pregnant when presented with the same males or artificial insemination techniques.

Two weeks following the breeding sessions, e.g. at 54 weeks, the two early cycling animals were unilaterally ovariectomized and the removed ovaries were sectioned for histological examination. The ovaries
20 appeared normal for this stage of follicular activity despite the functional infertility demonstrated.

Example 7

Vaccination With Porcine ZPC Protein

A purified porcine ZPC protein (ZP3 β) was obtained from E.
25 Yurewicz, prepared as described in *J. Biol. Chem.*, 262:564-571, (1987).

Vaccines were prepared by adding 167 μ g purified porcine ZPC protein (ZP3 β) to a 50/50 water-oil emulsion with complete Freund's adjuvant (Sigma No. F5881, St. Louis MO), for the priming dose or with Incomplete

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Freund's Adjuvant (Sigma No. F5506, St. Louis, MO) containing MDP as described in Example 6 for the booster doses.

Five random breed dogs of approximately 10-12 weeks of age were injected with the ZPC vaccine preparation described above using the regimen described in Table 3.

TABLE 3

			<u>mg of ZPC</u>
	Prime	Time 0	0.167
	Boost	Week 3	0.167
10	Boost	Week 6	0.167
	Boost	Week 28	0.167

Each animal's antibody titer versus self- zona proteins, e.g., versus canine zona pellucida proteins, was monitored by ELISA, using the method described in Dunbar, *Two Dimensional Gel Electrophoresis and Immunological Techniques*, 1987. ELISA microtiter plates were coated with HSDZ in antigen-coating buffer (0.1M sodium carbonate, pH 9.6). Biotinylated rabbit-antidog IgG was used as the second antibody. ABC reagent (Avidin-biotinylated peroxidase complex) and O-phenylene diamine dihydrochloride with a peroxide substrate was used for visualization. Only two animals produced antibodies versus self achieving peak self-antibody titers of 16K by week 4. The other three animals produced no self-antibody titers but achieved peak antibody titers of 4K against porcine zona pellucida protein. During the period of time between week 20 and week 36, all dogs were observed to exhibit estrous behavior. The animals were bred repeatedly with proven males. Only the two animals having antibody titers versus self zona pellucida proteins remained infertile. All other animals in the study became pregnant.

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Two weeks after estrous and breeding the two infertile dogs exhibiting self-antibody titers were unilaterally ovariectomized and the removed ovaries were sectioned and stained with PAS for histological examination. The histological examination revealed abnormal morphology in the ovaries of the infertile dogs. No evidence of ongoing folliculogenesis was seen and the ovaries were depleted of oocyte-containing follicles. In addition, no primordial oocytes were seen.

Example 8

Western Analysis of Antisera Produced by Vaccinated Animals

10

In an attempt to better understand the immune response and different physiological effects obtained in the two studies described in Examples 6 and 7, antisera produced in each test group was analyzed by Western Analysis against a variety of antigens including natural porcine ZPC, heat-solubilized dog zona pellucida (HSDZ), recombinant dog ZPA and ZPC, and recombinant pig ZPC. Western blots were probed with antiserum obtained from the test animals of Example 6, e.g., animals immunized with isoelectric focused, heat-solubilized porcine zona pellucida, and with antiserum obtained from the two test animals of Example 7 which contained antibodies against self-zona proteins.

15
20

The data demonstrate no recognition of recombinant porcine or canine ZPC by antisera from infertile, but cycling dogs immunized with heat solubilized porcine zona pellucida which contained no demonstrable ZPC by PAGE analysis, however, natural ZPC, HSDZ and recombinant canine ZPA were recognized. In contrast, antisera obtained from infertile dogs whose ovaries were depleted of oocytes recognized recombinant ZPC protein, i.e., the polypeptide backbone.

25

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A key difference in the antibody recognition of antigen was that only the antisera obtained from dogs having ovaries devoid of oocytes appeared to recognize the recombinant dog ZPC antigen. Infertile dogs whose antisera strongly recognized natural ZPC, HSDZ, and recombinant dog ZPA demonstrated no recognition of recombinant dog ZPC.

Given that autoimmunity is essential for a contraceptive effect, these data suggest that infertility without histologically evident ovarian dysfunction can be obtained in dogs via an autoimmune response against dog ZPA antigens. In contrast, histologically confirmed ovarian dysfunction, i.e., loss of oocytes, which would result in permanent sterility, requires the generation of antibodies which specifically recognize homologous species ZPC protein.

Example 9

Expression of Recombinant ZP Proteins

I. Construction of Expression Vectors

The plasmid vector pZ90 shown in Fig. 1 was constructed from fragments of the plasmids pUC9 (Vierra & Messing, *Gene* 19:259-268 (1982)) and p β gal2 (Queen, *J. Mol. App. Gen.* 2:1-10 (1983)). The single Pvu II restriction site present in p β gal2 was converted to a Sal I site using a Sal I polylinker adaptor purchased from New England Biolabs. The DNA sequences between the new Sal I site and a pre-existing Sal I site were excised by digestion with Sal I, religated and screened for the reduced size plasmid.

A Cla I - Nde I fragment of the modified p β gal2 plasmid which carried the λ CI repressor gene, the λ pR promoter and the Lac Z gene (β -galactosidase) was inserted into pUC9 between its Acc I and Nde I restriction sites. The pUC9 plasmid carries the ampicillin resistance (Amp^R) gene and col EI replication origin (ori) needed to maintain the plasmid in *E. coli* cells. The combination plasmid was further modified to convert the Bam

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HI site 3' of the ATG initiation codon (ATG GAT CCN) to a Bgl II site 5' of the ATG initiation codon (AGATCTATG). This was accomplished by partially digesting the plasmid with Rsa I. One of the several digestion points was about 20 bps 5' of the Bam HI restriction site. When the partially
5 digested plasmid was digested with Bam HI, some of the plasmids produced were nearly full length. A synthetic oligomer (GTACTAAGGAAGATCTATGGATCC) (SEQ ID NO. 29) was produced to replace the sequence that had been removed (GTACTAAGGAGGTTGTATGGATCC) (SEQ ID NO. 30). The net effect
10 of this replacement was the substitution of 3 bps to create the Bgl II restriction site. A DNA fragment containing approximately 3000 base pairs of the Lac Z gene was then excised by restriction digestion with Bgl I and Ban II and was followed by insertion of a synthetic oligomer containing a Bam HI site. The plasmid was cut with Bgl I and Ban II, and then treated with nuclease S1
15 to create blunt ends. A Bam HI linker (New England Biolabs) was inserted at the blunt ends of the digested plasmid. Next a Pvu II restriction site between the λ CI repressor gene and the ori sequence was converted to a Hind III site using a synthetic linker. The Pvu II restriction site was cut with Pvu II, and a Hind III linker (New England Biolabs) was ligated to the blunted
20 ends. Because the remaining lac Z sequence was missing the first 8 codons of the natural sequence, these 8 codons were replaced by synthesizing a synthetic oligomer that began with a Bgl II site and encoded the lac Z wild type gene product (β gal) N-terminal sequence.

The synthetic oligomer was prepared by synthesizing four
25 oligomers having the sequences set out in SEQ ID NO. 31 (oligomer 1), SEQ ID NO. 32 (oligomer 2), SEQ ID NO. 33 (oligomer 3), and SEQ ID NO. 34 (Oligomer 4). Oligomers 2 and 3 were phosphorylated by treating with kinase and ATP to add phosphate to the 5' end. Oligomers 1 and 2 were then hybridized to oligomers 3 and 4, respectively, by incubation at 100°C followed
30 by a slow cooling in 200 μ M NaCl. The resultant oligomer had the sequence

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set out in SEQ ID NO. 35. The synthetic oligomer as set out in SEQ ID NO. 35 had Bgl II-Pvu II ends and was substituted for the Bgl II-Pvu II sequence of the plasmid by restriction digestion of the plasmid and ligation with the oligomer.

5 The resultant plasmid was termed pZ90 and is shown in Figure 1. The plasmid pZ90 can be used to express recombinant proteins by heat induction, using the heat labile λ CI repressor. The heat-inducible repressor and promoter of pZ90 was next replaced with the chemically inducible promoter ptac (Amann *et al.*, *Gene* 25:167-178 (1983)). The ptac promoter
10 is controlled by the lac repressor, a product of the lac I gene (Farabaugh, *Nature* 279:765-769 (1978)). The Lac I gene was obtained from pMC9 (Miller *et al.*, *The EMBO Journal* 3:3117-3121 (1984)) by use of PCR methodology as described by Innis and Gelfand, In: *PCR Protocols: A Guide to Methods and Applications*, Innis, M.A., Gelfand, D.H., Sninsky, J.J. and
15 White, T.J. (eds.), pgs 1-12, Academic Press, Inc., San Diego, CA. The primers used were complimentary to the Lac I promoter at one end and the Lac I gene termination codon at the opposite end. The N-terminal primer carried a Hind III site and the C-terminal primer carried a tac promoter sequence followed by a Bgl II site. The N-terminal primer had the sequence
20 set out in SEQ ID NO. 36. The C-terminal primer had the sequence as set out in SEQ ID NO. 37 which includes a Dra 3 site having the sequence 5'-CACAATGTG-3'. The resulting lac I - ptac DNA fragment having Hind III and Bgl II restriction sites at its respective ends was then used to replace the Hind III - Bgl II fragment of pZ90 which carried the λ CI repressor and λ pR
25 promotor. This replacement yielded the plasmid pZ98 shown in Fig. 2.

II. Insertion of Recombinant ZP DNA

DNA sequences encoding porcine ZPC were prepared by the PCR procedures described above (Innis & Gelfand) from the plasmid pZ57 prepared in Example 1, which contains the full length porcine ZPC sequence

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obtained from λ gt11 clone 5-1 described for Example 1. During the PCR procedure the porcine ZPC gene was modified by using primers that did not include the leader sequence and the hydrophobic tail. The N-terminal primer used had the sequence set out in SEQ ID NO. 38 which included an internal
5 Bam HI restriction site having the sequence 5'-GGATCC-3'. The C-terminal primer used had the sequence as set in SEQ ID NO. 39 includes a Sal I restriction site having the sequence 5'-CTCGAG-3' and an internal Xho I restriction site having the sequence 5'-CTCGAG-3'. The modified ZPC gene contained base pairs 105 to 1154 encoding ZPC amino acids 1-350.

10 To the 5' end of the modified porcine ZPC gene was added a Bam HI restriction site, and to the 3' end was added an Xho I site, a Hexa-CAT-codon sequence (CAT)₆, a termination codon, and a Sal I restriction site. This modified porcine ZPC gene was inserted into the Bam HI - Sal I restriction site of pZ98 to yield the porcine ZPC expression vector,
15 plasmid pZ156 shown in Fig. 3. The (CAT)₆ sequence produces a C-terminal hexahistidine (His₆) amino acid sequence in the recombinant fusion protein which permits purification of the fusion protein by immobilized metal in affinity chromatography.

In a similar manner as described above, the plasmid pZ156
20 when digested with Bam HI and Xho I, may be used to receive any other recombinant ZP gene or gene fragment for expression as a β gal fusion protein which can be purified by metal ion affinity chromatography.

III. Expression of Porcine ZPC Fusion Protein in *E. coli*

The expression vector pZ156 (Fig. 3) was transformed into *E.*
25 *coli* strain Top 10F' (Invitrogen, San Diego, CA) by the procedure of Chung *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 2172-2175 (1989). The transformed *E. coli* cell line was termed Strain ZI 156, and was used to express recombinant porcine ZPC- β gal fusion protein.

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Bacterial cultures of ZI 156 were grown in Luria Broth (LB) containing 100 μ g/ml ampicillin at 30°C until the cell density reached an OD⁶⁰⁰ of approximately 1.5. Isopropyl beta-D-thiogalactopyranoside (IPTG) (3ml of 100mM solution/ 1 media) was added to induce expression from the tac promoter, and the cells were further incubated at 30°C for 2-3 hours. The cells were harvested by centrifugation, and the resulting cell pellet was frozen at -70°C.

The frozen cell pellets were suspended in 10 mM EDTA (1g/2-2.5 ml) and twice sonicated at 50% power for 3 minutes, cooling in an ice bath between each sonication. The cell lysate was then centrifuged at 3300 x g for one hour and the hard pellet was retained. This lysis procedure was repeated using the hard pellets.

In order to remove residual EDTA, the final hard cellular pellet was dispersed in a small volume of water by a brief burst of sonication, the suspension was centrifuged, and the supernatant discarded. The washed pellet was thoroughly resuspended in Buffer A, (6M guanidine hydrochloride (GuHCl), 100 mM Na H₂PO₄, 10 mM TRIS pH 8, at approximately 0.5 ml per original gram of cell pellet). The suspension was centrifuged at 10,000 x g for 45 seconds and the supernatant was retained while the pellet was discarded.

The retained supernatant was loaded onto a Ni column (in Buffer A) and the column was washed with 10 column volumes of Buffer A. The column was next washed with 5 volumes each Buffers B-D, each containing 8M urea, 100mM NaH₂PO₄, and 10 mM TRIS, and having successively reduced pH values of 8, 6.3, 5.9 for Buffers B, C, and D, respectively. The recombinant pZPC- β gal fusion protein eluted with Buffer E, at pH 4.5 as shown by screening by Western Blot analysis using rabbit anti-HSDZ and anti-HSPZ as probes. Further elution may be accomplished using Buffer F (pH 2.5) (8M GuHCl, 200 mM Acetic Acid).

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The fusion protein obtained by this protocol was prepared in its final dose for injection into a host animal by adjusting the final volume to 0.5 ml in 8M urea, and adding it to 0.5 ml adjuvant as described above. Each dose was injected subcutaneously into a test animal.

5

Example 10**Vaccination of Dogs with Recombinant
ZPC- β gal Fusion Protein**

Eleven mixed breed dogs approximately 5-6 months of age were randomly selected from test animals previously treated at approximately 2
10 months of age with heat solubilized porcine zona pellucida or chromatographically purified porcine ZP3 β in combination with various biopolymers as adjuvants and drug releasing vehicles. Six weeks post first injection, i.e., three and a half months of age, all test animals had achieved antibody titers versus HSPZ in the range of 2-16K as determined by ELISA.
15 However, none of the test animals achieved antibody titers against self-antigen, e. g., HSDZ.

At 5-6 months of age, five of the test animals were then injected with a loading dose of the porcine ZPC- β gal fusion protein prepared as described for Example 9. The recombinant ZPC- β gal fusion protein
20 produced in Example 9 was adjusted to the desired dose in a final volume of 0.5ml 8M urea and combined with 0.5 ml adjuvant. The adjuvant, N-acetyl-D-glucosaminyl- β (1,4)-N-acetyl muramyl-L-alanyl-D-isoglutamine (GMDP), 250 μ g, was dispersed in 0.42 ml mineral oil, 0.157 ml L-121 block polymers, and 0.02 ml Tween 80. Each dose was injected subcutaneously
25 into the five test animals. The remaining 6 animals were maintained as controls.

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Following a total of four injections given at 2-3 week intervals, antibody titers versus self antigen, e.g., HSDZ, were obtained in all test animals, with peaks in the range of 2-8 K as measured by ELISA.

Some of the control animals began to cycle beginning at approximately 9 months of age, and by 11 months of age, 4 of 6 control animals had experienced their first estrus. In contrast, none of the 5 test animals which had received recombinant ZPC- β gal fusion protein had cycled during this same time period. However, although the first estrus was delayed for several months in the test animals, they eventually began to cycle. Two of the five vaccinated dogs became pregnant during their second estrus after immunization while a third dog became pregnant during its third estrus after immunization; however, the two remaining test animals remain infertile through three estrus cycles and nearly two years after vaccination.

Example 11

Isolation of Human DNA Sequences Encoding Human Zona Pellucida Proteins ZPA and ZPB

A human genomic DNA library purchased from Stratagene (catalog no. 946203) was used for the isolation of DNA sequences encoding human ZP proteins. The library consisted of 9-23 kb inserts of human DNA (from placenta tissue of a male caucasian) cloned into the Lambda FixTMII vector (Stratagene). Approximately 40,000 pfus were plated on *E. coli* strain LE 392 (Stratagene, catalog no. 200266), as described in the Stratagene protocol, but replacing MgSO₄ with MgCl₂. After overnight incubation, nylon membrane lifts of the plaques were prepared and screened with ³²P-labelled porcine ZPA cDNA (SEQ ID NO. 1) and with ³²P-labelled porcine ZPB cDNA (SEQ ID NO. 3) as described in Example 2.

Three clones 1-1, 2-2, and 4-9 were shown to hybridize to the porcine ZPB cDNA (SEQ ID NO. 3). Clones 1-1 and 4-9 were deposited

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with the American Type Culture Collection, (ATCC) 12301 Parklawn Drive, Rockville, Maryland, on January 27, 1993 under ATCC Accession Nos. 75406 and 75405, respectively. Human DNA inserts were isolated from these clones and analyzed by restriction endonuclease digestion with Eco RI and Southern blot analysis as described in Example 1. Table 4 shows the results of Eco RI digestion of these clones.

Table 4
HUMAN GENOMIC ZPB EcoRI INSERTS

CLONES			
Fragment	1-1	2-2	4-9
A		2.8 kb	2.8 kb
B	2.2 kb		
C	2.0 kb		
D	1.5 kb		1.5 kb
E	0.2 kb		0.2 kb
F	3.2 kb	3.2 kb	3.2 kb
G	0.7 kb		

Southern blot analysis revealed four Eco RI fragments which were judged to carry ZPB coding sequences based on hybridization to the porcine ZPB cDNA (SEQ ID NO. 3). Clone 1-1 DNA included a 2.2 kb, 2.0 kb, and 1.5 kb Eco RI fragments which so hybridized. Clone 2-2 DNA included a 2.8 kb Eco RI hybridizing fragment. Clone 4-9 DNA included a 2.8 kb and a 1.5 kb Eco RI fragment which hybridized to the porcine ZPB cDNA probe. All inserts additionally included a 3.2 kb non-hybridizing Eco RI fragment; inserts from clones 1-1 and 4-9 both provided 0.2 kb non-hybridizing fragments; and clone 1-1 additionally provided a 0.7 kb non-hybridizing fragment.

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Further restriction analysis revealed the fragment alignment shown in Figure 4. Six of the fragments (A-F) were subcloned into pBSKS for sequence analysis, as described in Example 1. Preliminary sequence analysis confirmed the fragment alignment shown in Figure 4, and suggested
5 that the complete coding sequence of the human ZPB gene may be from clones 1-1 and 4-9. This was confirmed by nucleotide sequence analysis of the inserts, and comparison of the sequences with the feline ZPB sequence (SEQ ID NO. 15) and porcine ZPB sequence (SEQ ID NO. 3). The DNA sequence and deduced amino acid sequences for human ZPB are set out as
10 SEQ ID NO. 40 and 41, respectively.

Clones hybridizing to the porcine ZPA cDNA (SEQ ID NO. 1) under the conditions described in Example 1 were also isolated. Two positive clones, A1 and A4 were identified. The clones were deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville,
15 Maryland 20852, on January 27, 1993 under ATCC Accession Nos. 75404 and 75403 respectively. Southern blot analysis revealed that these clones contain all or part of the human ZPA gene. DNA was isolated from these clones and was analyzed by Bgl II, Hind III, and Not I restriction endonuclease digestion and Southern blot analysis as described in Example 1.
20 The size of the A1 clone DNA insert is approximately 11.6 kb, and that of the A4 clone is approximately 13.2 kb. Two of the Bgl II fragments which hybridized with the porcine ZPA cDNA (SEQ ID NO 1) were subcloned into pBSKS for sequence analysis, as described in Example 1. Sequence analysis revealed that A1 and A4 collectively contain the human ZPA gene as
25 supported by comparison to sequences with the porcine ZPA cDNA (SEQ ID NO. 1) and the canine ZPA cDNA (SEQ ID NO. 11). The complete DNA sequence and the deduced amino acid sequence are set out as SEQ ID NOS. 42 and 43, respectively.

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Example 12**Isolation and Sequencing of DNA Encoding****Cynomolgus Monkey ZPA, ZPB, and ZPC**

Cynomolgus monkey cDNA libraries were constructed in λ gt10 as described below. Briefly, a set of ovaries were collected from two female cynomolgus monkeys aged 1.5 years and 2 years, and a second set from three females aged 3 years, 4 years, and 14 years of age. Messenger RNA was isolated using the Fast Track™ mRNA isolation kit following the manufacturer's instructions. The cDNA was prepared using the Lambda Librarian™ (Invitrogen, as described in Example 2) kit following the protocol provided with the kit. The cDNA was packaged into lambda phage heads using the Proclone® (Promega, Madison, WI) λ gt10 *EcoRI* arms plus the Packagene® (Promega) lambda DNA packaging system following the manufacturer's instructions. This procedure generally produced libraries with a titer of greater than 1×10^6 pfu/ml. The monkey cDNA library was then screened using porcine ZPA, ZPB, and ZPC probes isolated from the porcine cDNA as described in Example 1. Screening was accomplished by preparing duplicate plaque lifts using Nytran® nylon filters (0.2 μ m pore size). The filters were prehybridized in a solution of 5x SSPE (43.83 g/l of NaCl, 6.9 g/l of NaH_2PO_4 , H_2O , 1.85 g/l of EDTA, pH 7.4), 5x Denhardt's Reagent (1 g/l of Ficoll [type 400], 1 g/l of polyvinylpyrrolidone and 1 g/l bovine serum albumin), 100 μ g/ml sonicated, denatured salmon sperm testes DNA, 30% formamide, and 0.5% SDS, for 3 hrs. at 42°C. Radio-labelled probes were prepared using [α - ^{32}P] -dATP and the Prime-a-Gene® (Promega) labelling system. After prehybridization, 10 ng of freshly radio-labelled probe was heat denatured at 95°C for 5 minutes in 50% formamide and 100 μ g/ml sonicated, denatured salmon testes DNA, and was added to the filters. The hybridization was carried out at 42°C for 15-24 hours. The hybridized filters were then washed twice with 100 ml of 5X SSPE at 55°C, for approximately one hour

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each wash. The filters were then rinsed in 250 ml of 5X SSPE at 55°C and allowed to air dry. The dried filters were exposed to x-ray film (Kodak XAR5, Eastman Kodak, Rochester NY) at -70°C using two intensifying screens (Kodak X-OMATIC™) for at least eight hours. The film was then developed for visual analysis.

Exhaustive screening of the two cynomolgus monkey ovarian cDNA libraries using all of the porcine probes yielded a total of 12 candidate clones. Southern hybridization revealed that only one of these clones (λ CM 4-2) hybridized to the porcine ZPA probe. This clone contained an insert of 560 bp. Sequencing of the insert was performed using the Sequenase® Version 2 kit (U.S. Biochemicals, Cleveland, Ohio) according to the manufacturer's instructions. Sequencing revealed that the 560 bp insert was homologous to the 3' end of other mammalian ZPA genes. The 560 bp fragment represents just under 25% bp of the full-length sequence and contains an open reading frame of 492 bp which would encode a protein of 164 amino acids. The DNA sequence and the deduced amino acid sequence of the cynomolgus monkey ZPA cDNA is set out as SEQ ID NOS. 44 and 45, respectively.

Exhaustive screening of the cynomolgus monkey ovarian cDNA libraries with the porcine ZPB probe yielded a single ZPB candidate clone having an insert of 866 bp. Sequence analysis suggests that the insert includes the C-terminal 50% of the expected full-length sequence. The DNA sequence and deduced amino acid sequence of the monkey ZPB insert are set out as SEQ ID NOS. 46 and 47, respectively. Screening of monkey ovarian cDNA libraries with the porcine ZPC DNA probe yielded only partial ZPC clones, the largest (λ CM1-1) having an insert of approximately 1300 bp which contains just over 50% of the C-terminal portion of the full-length sequence based on comparison to known ZPC clones, (particularly the human ZPC clone). The clone contains an open reading frame of 672 bp which would encode a protein of 224 amino acids. The clone also contains stop codons

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immediately 5' to the coding sequence in all three reading frames. The DNA sequence and the deduced amino acid sequence of the cynomolgus monkey ZPC clones are set out as sequence ID NOS 48 and 49 respectively.

Example 13

5 Comparison of ZPA DNA and Deduced Amino Acid Sequences

Table 5 shows a comparison of the DNA and deduced amino acid sequence of mammalian ZPAs.

TABLE 5
ZPA HOMOMOLOGY

		PROTEIN HOMOMOLOGY							
		Mouse	Rabbit	Pig	Cow	Dog	Cat	Monkey	Human
Mouse	--	--	61.0%	54.2%	60.8%	57.9%	56.9%	57.2%	58.9%
Rabbit	73.0%	--	--	63.0%	69.8%	66.2%	64.6%	65.1%	68.9%
Pig	69.0%	75.6%	--	--	79.9%	69.6%	70.2%	56.9%	63.9%
Cow	70.5%	79.0%	86.2%	--	--	78.3%	77.8%	59.0%	63.6%
Dog	70.4%	77.2%	80.4%	84.8%	--	--	83.1%	66.9%	67.5%
Cat	69.6%	77.5%	81.3%	84.7%	88.9%	--	--	65.5%	67.4%
Monkey	56.7%	59.6%	56.6%	57.0%	59.2%	58.4%	--	--	95.8%
Human	68.4%	74.6%	73.7%	63.1%	74.4%	75.3%	96.3%	--	--

DNA HOMOMOLOGY

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Data is presented as a cross-wise comparison of the ZPA protein and DNA sequences. The comparison of the protein sequences are shown in the upper right hand side of the table, above the diagonal dashed lines. The comparison of the DNA sequences are shown in the lower left hand side of the table, below the diagonal dashed lines. The ZPA DNA and deduced amino acid sequences are highly homologous between species. The homology is highest between members of the same order within the class *mammalia*. For example, the human and cynomolgus monkey (*primata*), the pig and cow (*ungulata*), and the cat and dog (*carnivora*) sequences have the most similarity. The high degree of homology between the ZPA genes, as well as between the ZPB (see Example 14) and ZPC (Example 15) genes from a variety of mammalian species, implies a great deal of structural similarity in the ZP layers of these species. However, post-translational modification differences such as glycosylation and others, could represent a potential source of variation.

One protein processing site that all of these ZPA proteins have in common is a furin cleavage site (R-X-R/K-R; Hosaka *et al. J. Biol. Chem.*, 266:12127 (1991)) near the C-terminal end of the protein. In fact, with only a few exceptions, all ZP proteins contain a furin processing site near the C-terminus. This furin site could serve to cleave off a putative membrane anchor sequence which would allow the processed proteins to move toward the outer edge of the growing ZP layer.

The human ZPA gene contains an exon near the 3' end that is present in the cynomolgus monkey ZPA sequence, but not present in the ZPA genes from other species. This extra exon codes for an amino acid sequence that occurs after the furin processing site, which suggests that the C-terminal fragment generated by furin cleavage might still be important to the function of the ZP layer or to the oocyte in some way.

There are 20 conserved cysteine residues and one or two non-conserved cysteine residues in each of the full-length ZPA sequences. The

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non-conserved cysteine residues occur either in the N-terminal leader sequence region, or in the extreme C-terminal region of the sequence, where a large amount of the variation between the ZPA sequences occurs. The high degree of homology and the large number of conserved cysteine residues suggests that
5 the tertiary structures of the ZPA proteins are similar.

It has been noted previously that there are regions of homology between the ZPA and ZPB class proteins (Schwoebel *et al. J. Biol. Chem.*, 266:7214 (1991); Lee *et al. J. Biol. Chem.*, 268: 12412 (1993); Yurewicz *et al. Biochem. Biophys. Acta* 1174:211 (1993)). Comparison of the human
10 ZPA genomic structure with the human ZPB genomic structure shows these regions to be confined to exons 12, 13, and 14 of the human ZPA gene and exons 5, 6, and 7 of the human ZPB gene. This suggests that this homology might be due to a partial ancestral gene duplication. The ZPB proteins contain 21 conserved cysteine residues. The first 11 of these do not align
15 with those in the ZPA proteins, but the last 10 match well. This extends the homology to approximately 270 amino acids, covering exons 11-16 of the ZPA gene and exons 4-9 of the ZPB gene, although the overall homology of the expanded region is slightly lower (approximately 43%). The remainder of the ZPA and ZPB genes show very little homology with each other, and the
20 ZPC genes also show no extensive homology to the ZPA genes. In addition, the ZPA gene has no extensive sequence similarity to non-ZP nucleic acid and protein sequences in Genbank and the SwissProt data banks.

Example 14

Comparison of ZPB DNA and of Deduced Amino Acid Sequences

25 Table 6 shows the comparison of the six known ZPB DNA and protein sequences (the bovine and cynomolgus cDNA fragments are only compared to the corresponding regions of the other full-length ZPB sequences).

TABLE 6

ZPB HOMOLOGY

PROTEIN HOMOLOGY

	Rabbit	Bovine	Porcine	Feline	C. Monkey	Human
Rabbit	--	75.3%	65.3%	60.1%	70.2%	65.2%
Bovine	78.8%	--	82.3%	71.2%	69.9%	69.6%
Porcine	74.2%	86.2%	--	63.7%	63.6%	63.1%
Feline	69.5%	78.7%	72.9%	--	70.3%	64.6%
C. Monkey	78.9%	78.5%	78.2%	78.6%	--	92.3%
Human	74.3%	80.8%	73.3%	74.2%	95%	--

DNA HOMOLOGY

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The data are presented as cross-wise comparison of the ZPB protein and DNA sequences. The comparison of the protein sequences are shown in the upper right hand side of the table, above the diagonal dashed lines. The comparison of the DNA sequences are shown in the lower left hand side of the table, below the diagonal dashed lines.

The data shows considerable ZPB homology among members of different mammalian species. As was the case with ZPA, this homology is most pronounced between members of the same order within the class *mammalia*. For example, the human and cynomolgus monkey sequences (*primata*) and the pig and cow sequences (*ungulata*) have the most homology to each other. With only a few exceptions (noted below), the ZPB sequences show no homology to other DNA or protein sequences in the GenBank or SwissProt databases. Hybridization experiments suggest that the ZPB transcripts are ovary specific.

Comparisons of the deduced amino acid sequences of the ZPB clones show more divergence within this genetic group than within the ZPA and ZPC groups. Comparison of the rabbit ZPB and porcine ZPB shows the sequences to be predominantly collinear (74% homologous) except that the rabbit has an additional upstream ATG codon which adds six codons to the rabbit sequence.

The feline ZPB sequence has two additional amino acid inserts, which total 38 additional codons, in the first quarter of the gene, compared to the porcine and rabbit sequences. Both inserts occur just after cysteine residues, which suggests that if the cysteines are involved in disulfide bridges, these regions might form unique epitopes. However, the feline gene is still 73% homologous to porcine gene and 70% homologous to the rabbit gene.

The human gene has a sequence homologous to the first of the inserts in the cat sequence, but not the second. However, there are consensus splice site donor and acceptor sequences adjacent to this extra region in the human sequence, which if used would leave the coding sequence in frame.

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Therefore, the sequence representing exon 2 could actually be two small exons (122 and 103 bp), separated by a small intron (84 bp). This would make the human sequence in this region identical to the pig sequence. The first extra region in the cat sequence is also flanked by in frame splice site donor and acceptor signals. If the extra region was removed from the cat sequence, it would differ from the pig sequence by only a single amino acid. However, the cat sequence was obtained from a cDNA clone made from an mRNA that appears to be fully processed. The second extra region in the cat sequence does not contain in frame splice site donor or acceptor signals, and therefore is probably not due to the presence of an unprocessed intron.

The cynomolgus monkey and human sequences have an additional seven codons at the C-terminus when compared to the other ZPB sequences. In the cynomolgus monkey, this is due to a two-base pair deletion, which causes a frameshift mutation which puts the termination codon used by the other species out of frame. The human sequence also contains this deletion, but in addition, there is also a base change that eliminates this termination codon.

There are 21 conserved cysteine residues in the ZPB proteins, the final 10 of which occur in a region that has homology to the ZPA proteins. This homology was noted previously (Schwoebel *et al.*, *supra*; Lee *et al. supra*, 1993; Yurewicz *et al. supra*, 1993), but examination of the genomic structure of the human ZPA and ZPB genes allowed the homology to be extended to approximately 270 amino acids. This homology could be due to a partial ancestral gene duplication. In addition to the conserved cysteine residues, the pig ZPB protein contains one additional cysteine residue in the putative leader sequence, and the human sequence contains four additional cysteine residues. The first of these is in the putative leader sequence (in a different location than pig), the second is in the region containing the additional insert, and the last two are in the C-terminal

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extension caused by the mutated termination codon. These last two extra cysteine residues are conserved in the cynomolgus monkey sequence.

All of the ZP proteins contain a putative transmembrane domain near the C-terminus. However, the canonical furin proteolytic processing signal (R-X-R/K-R, Hosaka *et al. supra*, 1991), which occurs just prior to the transmembrane domain in all of the ZPA and ZPC proteins, is altered in the human (S-R-R-R), cynomolgus monkey (S-R-R-N) and rabbit (S-R-R-R) ZPB sequences. The significance of this is unknown, but it may indicate that these proteins are processed by a related system with specificity for di- or tribasic sequences, since the release of the putative transmembrane domain would be necessary for the ZPB protein to move as the ZP layer grows. There appears to be a great deal of proteolytic processing of the pig ZPA and ZPB (Yurewicz *et al. supra*,) proteins. There is no data concerning the post-translational modification of the ZPB proteins of cat, cow, cynomolgus monkey or human. The physiologic significance of this processing is unknown, but differential processing would present an avenue of variation among species of the highly conserved ZP proteins.

There is a question of whether humans actually transcribe the ZPB gene. Since the amount of human ovarian mRNA recovered was so small, there was not enough RNA to both construct a cDNA library and perform a Northern analysis. However, since cynomolgus monkey transcribes the ZPB gene, it is probable that the highly homologous human ZPB gene is also transcribed.

The apparent lack of a ZPB cDNA in the dog cDNA library is another puzzle. All of the libraries screened which contained any zona pellucida gene contained all three genes, except the dog. However, mRNA isolated from the ovary of a six-month old dog (the library was made from the ovary of a four-month old dog), includes a ZPB mRNA that comigrates with the porcine and cynomolgus monkey ZPB mRNA on a Northern blot. One possibility to explain the lack of a canine ZPB cDNA is that the transcriptional

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timing of the three ZP genes is spread out, and since the ovary used to make the library was young, the transcription of the ZPB gene occurs later than the ZPA and ZPC genes (Andersen and Simpson, 1973).

Example 15

5 Comparison of ZPC DNA and Deduced Amino Acid Sequences

Table 7 shows the comparison of the DNA and deduced amino acid sequences from all of the ZPC cDNAs and genes.

TABLE 7

ZPC HOMOMOLOGY

PROTEIN HOMOMOLOGY

	Mouse	Hamster	Rabbit	Pig	Cow	Dog	Cat	Monkey	Human
Mouse	--	78.8%	65.9%	65.6%	64.0%	64.7%	63.3%	64.4%	67.0%
Hamster	84.7%	--	65.9%	65.6%	63.5%	65.1%	63.6%	68.2%	68.0%
Rabbit	70.1%	71.3%	--	68.2%	68.5%	65.3%	64.1%	59.4%	68.5%
Pig	71.5%	72.0%	74.6%	--	83.6%	75.7%	72.8%	69.2%	73.7%
Cow	70.5%	71.4%	74.5%	86.5%	--	74.5%	72.8%	67.4%	71.1%
Dog	70.1%	71.9%	71.5%	79.8%	80.3%	--	79.2%	66.5%	70.1%
Cat	70.9%	71.6%	73.0%	79.3%	80.0%	84.3%	--	71.1%	70.5%
Monkey	72.4%	74.1%	71.3%	76.6%	77.2%	73.8%	77.8%	--	90.6%
Human	74.1%	75.0%	76.2%	80.0%	79.6%	77.7%	78.8%	94.4%	--

DNA HOMOMOLOGY

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The data are presented as a cross-wise comparison of the ZPC protein and DNA sequences. The comparison of the protein sequences are shown in the upper right hand side of the table, above the diagonal dashed lines. The comparison of the DNA sequences are shown in the lower left hand side of the table, below the diagonal dashed lines.

ZPC proteins and DNA sequences show a higher degree of homology than the ZPA and ZPB DNAs and proteins. As was the case with ZPA and ZPB, the homology is most pronounced in members of the same order within the class *mammalia*; the human and cynomolgus monkey sequences (*primata*), the cat and dog sequences (*carnivora*), the pig and cow sequences (*ungulata*), and the mouse and hamster sequences (*rodenta*). The ZPC transcripts are ovary specific, based on Northern blot analysis and comparison to the sequences in the GenBank and SwissProt databases detects no significant non-ZP homology. Comparison of the deduced amino acid sequences of the known ZPC genes detects three regions that contain large numbers of non-consensus sequences. These regions are: the putative leader sequences and the first 20-25 amino acids of the mature protein; the region containing the peptide that was identified as a sperm-binding region in the mouse (Millar *et al. Science* 216:935-938 (1989)); and the C-terminal region of the proteins that might be removed from the mature protein at the furin processing site (see below).

The epitope identified as a putative sperm-binding site (Millar *et al. supra*, 1989) occurs immediately before a furin proteolytic cleavage site (Hosaka *et al.*, 1991). The furin site (R-X-R/K-R) is highly conserved in all of the ZPC sequences. However, it should be noted that the canine ZPC sequence contains a second furin site, 19 amino acids upstream from the first furin site. Also as is the case with ZPA and ZPB, cleavage by furin of the ZPC proteins would remove a putative membrane anchor sequence (Klein *et al.*, 1985), which would allow the processed ZPC protein to move toward the outer layer of the expanding oocyte. Therefore, this sperm-binding site

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probably represents the C-terminus of the mature proteins. However, there is very little homology (even between hamster and mouse) in the regions of the ZPC proteins corresponding to this epitope. This might indicate that this region contributes to the species specificity of sperm-egg binding.

5 The variation that is seen at the C-terminus of the ZPC proteins occurs in the putative transmembrane region. This variation could indicate that this amino acid sequence is less important than the overall hydrophobicity of the amino acids in this region, similar to the lack of homology seen in leader sequences. However, it is also possible that this variation signifies a
10 species-specific function for this region.

Each ZPC sequence contains 14 conserved cysteine residues, but each sequence also has one or two extra cysteine residues that are shared only with one or a few other sequences. These extra cysteine residues are near the N- or C-terminus of the proteins, where the greatest sequence
15 variation exists. However, the large number of conserved cysteine residues probably indicates that the overall structure of the central core of all of these proteins is quite conserved.

Example 16

Immunization of Cynomolgus Monkeys With HSPZ

20 A sexually mature cynomolgus monkey was immunized with HSPZ to test the ability of HSPZ to induce infertility. HSPZ was prepared as described in Example 6. HSPZ was mixed with the following GMDP/oil adjuvant. 50 μ g GMDP (N-acetyl-D-glucosaminyl-(β 1-4)-N-acetylmuramyl-D-isoglutamine) (CC. Biotech, Poway, CA); 42.1 of mineral oil, 15.8% pluronic
25 VC-121 (block polymer polyols, BASF-Wyandotte, Parsippany, NJ). The animal received a series of 4 subcutaneous injections of 1 mg of HSPZ in the GMDP/oil adjuvant beginning with a priming dose followed four weeks later by a booster dose, which was followed by two booster doses five weeks apart

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which were followed six weeks later by a final dose. This dosage regimen resulted in an anovulatory monkey having antibody titers against its cynomolgus monkey heat-solubilized zona pellucida prepared as described for HSPZ. The peak antibody titers to cynomolgus monkey HSPZ were 1:8000-
5 1:16,000.

A fractionated preparation of HSPZ which is essentially native porcine ZPA and ZPB was prepared by isoelectric focusing, as described in Example 6 and was used to vaccinate cynomolgus monkeys using 1 mg of fractionated HSPZ in GMDP/oil injected subcutaneously according to the
10 following schedule: a priming dose was given followed approximately 6 weeks later by a booster dose followed by a final booster dose 11 weeks after the previous booster dose. The immunized monkeys achieved peak antibody titers of 1:4,000-1:8,000 against monkey heat-solubilized zona pellucida while maintaining a regular ovulatory cycle. However, despite maintaining a
15 regular ovulatory cycle, the monkeys remained infertile until their antibody titers to monkey heat-solubilized zona pellucida fell below 1:500 after which the animals became pregnant upon breeding.

Immunization of cynomolgus monkeys with recombinant baculovirus produced canine ZPC and porcine ZPC (prepared as described in
20 Example 18) failed to induce infertility despite inducing antibody production against monkey heat-solubilized zona pellucida. One possible explanation for this is that the glycosylation pattern of ZP proteins produced in the baculovirus system may prevent recognition of the epitopes responsible for induction of infertility.

25 Bacterially produced porcine ZPA, ZPB, and ZPC described above administered to cynomolgus monkeys failed to induce detectable antibody titers against cynomolgus monkey heat-solubilized zona pellucida even though antibody titers against the presented antigens were produced.

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Example 17**Mapping of Mammalian Zona Pellucida Protein Epitopes**

A Pin Technology™ Epitope Scanning Kit purchased from Chiron Mimotopes U.S., Emeryville, CA (Catalog No. PT-02-20000A) was
5 used for mapping epitopes in Zona Pellucida proteins. The procedures described in the kit manual were followed, with the exception of modifications in the ELISA testing procedure (described below).

Briefly, Pin Technology software was installed in a United Business Machines 486/33 computer according to the manufacturer's
10 instructions. The protein sequence was entered into the computer program, the desired peptide length, and degree of overlap between peptides were selected, and a protocol containing the daily requirements of activated protected amino acid derivatives and their location in the coupling tray wells was printed. Prior to use, the pins were first washed once with
15 dimethylformamide (DMF), and then with methanol three times, each wash lasting for two minutes. The pin block was air dried and the pins were deprotected by agitation in a 20% mixture of piperidine in DMF at room temperature for 30 minutes. The pins were washed again as described above, except that the washes were for 5 minutes each, and the pin block was then
20 air dried. The required amino acid derivative solutions were prepared and dispensed into the wells of the synthesis tray according to the protocol for the current cycle. The dried mimotope pins were washed once more in a DMF bath for 5 minutes and then positioned appropriately in the wells of the synthesis tray. The assembly was then sealed in a plastic bag and incubated
25 at 30°C for approximately 22 hours. On the following day, the pin block was removed from the coupling tray and subjected to the same cycle of washing, deprotection, and coupling steps as outlined above; however, using the amino acid derivatives and their tray location appropriate to the next cycle. The

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foregoing cycle of washing, deprotection, washing, and coupling was repeated until the peptide sequences were completed.

After coupling the terminal amino acids of the peptides, the pin block was washed, air dried, deprotected, washed and air dried as before.

5 The terminal amino groups of the peptides were then acetylated by immersion of the pins in a mixture containing 5 parts DMF, 2 parts acetic anhydride, and 1 part triethylamine, by volume, dispensed in the wells of a polypropylene coupling tray, and incubating at 30°C for 90 minutes. The pin block was removed, subjected to another washing sequence as before, and air dried.

10 Side chain deprotection of the peptides was performed by agitating the pin block in a mixture containing 95 parts trifluoroacetic acid, 2.5 parts anisole, and 2.5 parts ethanedithiol, by volume, at room temperature for 4 hours. The pin block was then air dried for approximately 10 minutes, sonicated in a bath containing 0.1% hydrochloric acid in a mixture containing
15 equal parts of methanol and deionized water, by volume, for 15 minutes, and finally air dried.

Prior to ELISA testing, the pins were subjected to a disruption procedure involving sonication in a bath consisting of a mixture containing 39 parts sodium dihydrogen orthophosphate, 25 parts sodium dodecyl sulfate, 0.1
20 part 2-mercaptoethanol, and 2500 parts deionized water, by weight, adjusted to pH 7.2 with 50% sodium hydroxide solution. The sonication was performed at 55 to 60°C for approximately 45 minutes. The pin block was then washed by immersion with gentle agitation in three sequential baths of deionized water at 60 degrees for three minutes each. Finally, the pin block
25 was immersed in gently boiling methanol for approximately 4 minutes and then air dried.

Preparation of Antisera

Antisera directed against zona pellucida proteins was prepared by immunizing the appropriate animals with the appropriate zona pellucida

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protein using procedures well known in the art and described in E. Harlow and D. Lane in *Antibodies, A Laboratory Manual*, Chapter 5, Cold Spring Harbor Laboratory, 1988 which is incorporated herein by reference. Biotinylated antisera was prepared by a modification of the procedure described in Harlow *supra* (page 314). Briefly, to a solution containing between 1 and 3 mg per ml of the selected antibody IgG fraction in phosphate buffer with saline (PBS) at pH 7.2 was added a solution containing 25 to 250 micrograms biotinamidocaproate, N-hydroxysuccinimide ester (Sigma, Cat No. B2643) in dimethyl sulfoxide at a concentration of 10 mg/ml. The mixture was mixed well and then incubated at room temperature for 4 hours. One molar ammonium chloride solution in the amount corresponding to 20 microliters per 250 micrograms biotin ester was added, and the resulting mixture was incubated at room temperature for 10 minutes. Unreacted biotin ester was then removed by extensive diafiltration with PBS using a Centricon-30 (TM) microconcentrator devices (Amicon Division, W.R. Grace & Co., Inc., Beverly MA). The dilution factor for the resulting conjugate was determined by ELISA titration against the appropriate native protein.

ELISA Testing

A modification of the procedure described in the Epitope Scanning Kit manual was employed.

After disruption, the mimotope pins were blocked by incubation with "supercocktail" (10 g ovalbumin, 10 g bovine serum albumin, and 1 ml Tween 20 detergent per liter of PBS) at room temperature for 1 hour. This was followed by incubation at room temperature for 2 hours with appropriately diluted biotinylated antisera. The pins were washed 4 times with PBS containing 0.5% Tween 20 (PBST) at room temperature for 10 minutes each time, with agitation.

The pins were then incubated at room temperature for 1 hour with the secondary antibody, horseradish peroxidase-streptavidin conjugate

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(Zymed Laboratories, Inc., South San Francisco, CA) diluted 1:2500 with PBST. They were washed again as described above.

Substrate buffer was prepared by combining 200 ml 1.0 M. disodium hydrogen orthophosphate solution with 160 ml 1.0 M. citric acid solution, diluting the mixture with 1640 ml deionized water, and adjusting to pH 4.0 using either citric acid or sodium hydroxide solutions. Substrate solution was prepared by dissolving 10 mg 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) diammonium salt in 20 ml substrate buffer and adding 6 microliters 30% hydrogen peroxide. The mimotope pins were incubated at room temperature with this solution, using microtiter plates containing 150 microliters per well. When color development appeared to be appropriate for measurement by an ELISA plate reader, the pin block was removed and the plate was read at a wavelength of 450 nm. The pin block was then disrupted by the procedure described above.

The data were entered into the Pin Technology™ computer program, which performed statistical analysis and evaluation and furnished a print-out of the results identifying the strongest binding epitopes. Briefly, the 25% of the wells having the lowest optical density readings were assumed to represent background in each experiment. The mean value and the standard deviation of these readings were calculated. Significant recognition of peptides by antisera was attributed to the pins corresponding to those wells showing absorbance readings greater than the sum of the background mean and three standard deviations from the mean.

Human ZPA epitopes were examined for reactivity with mouse anti-human ZP antiserum prepared as described above. Peptides of 15 amino acids in length were synthesized beginning with amino acid number 1 as illustrated in SEQ ID NO. 43. Successive peptides having a 7-amino acid overlap with the preceding peptide of the series were synthesized. The following peptides were shown to bind mouse anti-human ZP antiserum: 1-15, 9-23, 25-39, 33-47, 65-79, 81-95, 89-103, 97-111, 105-119, 113-127,

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121-135, 129-143⁴, 145-159, 153-167, 161-175, 193-207, 209-223, 217-231,
225-239, 241-255, 249-263, 273-287, 281-295, 289-303, 305-319, 313-327,
321-335, 329-343, 337-351, 345-359, 385-399, 393-407, 401-415, 409-423,
417-431, 425-439, 441-455, 449-463, 457-471, 481-495, 489-503, 497-511,
5 505-519, 513-527, 521-535, 537-551, 545-559, 561-575, 569-583, 577-591,
585-599, 601-615, 609-623, 617-631, 625-639, 633-647, 641-655, 665-679,
697-711, 705-719, 713-727, 721-735, and 729-743.

Similarly, human ZPB epitopes were mapped using mouse anti-human ZP antiserum. In these experiments, 15 amino acid peptides were
10 synthesized beginning with amino acid number 1 as set out in SEQ ID NO. 41. The overlap between successive peptides in this case was 9 amino acids. The following peptides were shown to bind mouse anti-human ZP antiserum:
7-21, 25-39, 31-45, 49-63, 67-81, 73-87, 79-93, 91-105, 103-117, 121-135,
193-207, 205-219, 211-225, 217-231, 223-237, 229-243, 253-267, 259-273,
15 265-279, 283-297, 289-303, 295-309, 301-315, 307-321, 313-327, 319-333,
343-357, 349-363, 355-369, 367-381, 373-387, 379-393, 385-399, 403-417,
409-423, 415-429, 421-435, 433-447, 439-453, 445-459, 451-465, 481-495,
487-501, 499-513, 505-519, 511-525, 523-537, 529-543, and 547-561.

Human ZPC epitopes were mapped using mouse anti-human ZP
20 antiserum. In these experiments, the 15 amino acid peptides were synthesized beginning with amino acid number 1 as set out in Chamberlin *et al.*, *Proc. Nat'l Acad. Sci. USA* 87:6014-6018 (1990) which is incorporated herein by reference. The overlap between successive peptides was 10 amino acids. The following peptides were shown to bind mouse anti-human ZP antiserum: 21-
25 35, 51-65, 116-130, 146-160, 151-165, 181-195, 241-255, 251-265, 271-285,
296-310, 321-335, 401-415, and 411-425.

Canine ZPC epitopes were mapped using rabbit anti-canine ZP antiserum. In these experiments, the 15 amino acid peptides were synthesized beginning at amino acid number 1 set out in SEQ ID NO. 10. The overlap
30 between successive peptides was 5 amino acids. The following peptides were

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shown to bind rabbit anti-canine ZP antiserum: 51-65, 61-75, 81-95, 131-145, 181-195, and 301-315.

Feline ZPC epitopes were mapped using rabbit anti-feline ZP antiserum. In these experiments, the 15 amino acid peptides were synthesized beginning at amino acid number 1 as set out in SEQ ID NO. 18. The overlap between successive peptides was 5 amino acids. The following peptides were shown to bind rabbit anti-feline ZP: 36-50, 46-60, 56-70, 76-90, 96-110, 106-120, 116-130, 126-140, 136-150, 146-160, 156-170, 186-200, 196-210, 246-260, 266-280, 276-290, 286-300, 296-310, 316-330, 326-340, 336-350, 346-360, 376-390, 396-410, and 406-420.

Bovine ZPC epitopes were mapped using rabbit anti-bovine ZP antiserum. In these experiments, the overlapping 15 amino acid peptides were synthesized beginning at amino acid number 1 as set out in SEQ ID NO. 24. The overlap between peptides was 10 amino acids. The following peptides were shown to be reactive with rabbit anti-bovine ZP antiserum: 1-15, 31-45, 51-65, 56-70, 61-75, 76-90, 106-120, 111-125, 116-130, 121-135, 131-145, 136-150, 141-155, 146-160, 151-165, 161-175, 181-195, 186-200, 191-205, 196-210, 201-215, 206-220, 216-230, 226-240, 241-255, 246-260, 261-275, 266-280, 271-285, 276-290, 291-305, 296-310, 301-315, 316-330, 321-335, 326-340, 331-345, 336-350, 341-355, 356-370, 361-375, 376-390, 381-395, 386-400, 396-410, 401-415, and 406-420.

Example 18

Immunization of Dogs with Recombinant ZPC Proteins

Dogs were immunized with various preparations of recombinant canine ZPC. The plasmid pZ169 bacterial expression vector (Figure 5) was constructed as follows. The parent vector pZ98 (described in Example 9) was digested with the restriction enzymes *PvuI* and *Bam* HI, and the large

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fragment was gel purified. Into this vector was ligated a fragment created by annealing the following oligonucleotides:

5' CGCCCTTCCCAGCAACTGCACCATCACCACCATGGG 3'
(SEQ ID NO. 50); and

5 5' GATCCCCATGGTGGTGGTGGTGGTGCAGTTGCTGGGAAGGGCGAT 3'
(SEQ ID NO. 51).

These oligonucleotides create a fragment with *PvuI* and *BamHI* ends, and codes for the hexapeptide sequence His₆. This intermediate vector was digested with the restriction enzymes *BamHI* and *EcoRI*, and the large
10 fragment was gel purified. Into this vector was ligated a fragment created by annealing the following oligonucleotides:

5' GATCCCTCGAGCCACCATCACCACCATCATG 3'
(SEQ ID NO. 52); and

15 5' AATTCATGATGGTGGTGGTGGTGGCTCGAGG 3'
(SEQ ID NO. 53).

These oligonucleotides create a fragment with *BamHI* and *EcoRI* ends and an *XhoI* site just downstream of the *BamHI* site, and which codes for the hexapeptide sequence His₆. This new vector was named pZ88, and contains unique *BamHI* and *XhoI* cloning sites between two His₆ sequences. To create
20 pZ169, the pZ88 vector was digested with the restriction enzymes *BamHI* and *XhoI*, and the large fragment was gel purified. Into this vector was ligated a fragment generated by performing a PCR (polymerase chain reaction) of the canine ZPC cDNA using the following oligonucleotides:

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5' CCCGGATCCGCAGACCATCTGGCCAACTGAG 3'
(SEQ ID NO. 54); and

5' GCGCTCGAGGGCATATGGCTGCCAGTGTG 3'
(SEQ ID NO. 55).

5 This PCR creates a fragment containing amino acids 23-207 of the canine ZPC sequence, with *Bam*HI and *Xho*I ends. This new vector is named pZ169, (Figure 5) and produces a protein containing amino acids 1-56 of the *E. coli* β -galactosidase sequence, His₆, amino acids 23-207 of the canine ZPC sequence, His₆, and amino acids 1006-1023 of the *E. coli* β -galactosidase
10 sequence. This protein is referred to as N-terminal canine ZPC. In Figure 5, pTAC refers to the tac promoter described above; AmpR refers to an ampicillin resistance marker, ori is an *E. coli* origin of replication sequences and pLacI is the lacI promoter which drives expression of the lacI gene.

Recombinant canine ZPC was produced and purified as
15 described in Example 9. A baculovirus expression vector pZ145 was constructed as follows. The parent vector pBlueBac2 (purchased from Invitrogen Corporation, San Diego, CA) was digested with the restriction enzymes *Nhe*I and *Bam*HI, and the large fragment was gel purified. Into this vector was ligated a fragment generated by a PCR of the porcine ZPC cDNA
20 using the following oligonucleotide:

5' CGCGCTAGCAGATCTATGGCGCCGAGCTGGAGGTTTC 3'
(SEQ ID NO. 56); and

5' CGCGGATCCTATTAATGGTGGTGATGGTGGTGACTAGTGGACCCTTCCA 3'
(SEQ ID NO. 57).

25 This PCR creates a fragment with *Nhe*I and *Bam*HI ends, and contains amino acids 27-350 of the porcine ZPC sequence followed by an *Spe*I site and the hexapeptide His₆. This new vector is named pZ147. To create the pZ145 vector, pZ147 is digested with *Nhe*I and *Spe*I and the large fragment is gel purified (this removes the pig ZPC sequence). Into this vector was ligated a

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fragment generated by a PCR of the canine ZPC cDNA using the following oligonucleotides:

5' CCCGCTAGCAGATCTATGGGGCTGAGCTATGGAATTTTC 3'
(SEQ ID NO. 58); and

5 5' CGCACTAGTTGACCCCTCTATACCATGATCACTA 3'
(SEQ ID NO. 59).

This PCR creates a fragment with *NheI* and *SpeI* ends, and contains amino acids 1-379 of the canine sequence. Transformants of this ligation were screened for the presence of the inserted *NheI/SpeI* fragment in the correct orientation (since the *NheI* and *SpeI* sticky ends are identical). This new vector is named pZ145, (Figure 6) and produces a protein containing amino acids 1-379 of the DZPC sequence followed by His₆. This protein is referred to as baculo-canine ZPC. In Figure 6, pP represents the baculovirus polyhedrin promoter, AmpR represents an ampicillin resistance marker, LacZ represents the gene for β -galactosidase, pE is a constitutive promoter which drives the expression of LacZ and ori is the *E. coli* origin of replication.

Recombinant baculovirus derived canine ZPC was produced by co-transfecting insect SF9 cells with pZ145 and *Autographica californica* multiply enveloped nuclear polyhedrosis virus (AcMNPV) using methods well known in the art as described in the MAXBAC™ kit purchased from Invitrogen, San Diego, CA. Recombinant canine ZPC produced in SF9 cells was prepared from cotransfected SF9 cells as follows. Cotransfected cells were harvested and pelleted by centrifugation and recombinant canine ZPC was purified as was described in Example 9 for purification from a cell pellet.

Recombinant canine ZPC may also be isolated from the culture medium and purified on a Ni-column as described in Example 9.

Other expression vectors which are capable of expressing zona pellucida encoding nucleotide sequences under the control of a variety of

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regulatory sequences are within the scope of the present invention and are readily constructed using methods well known in the art.

Recombinant zona pellucida proteins may also be modified to increase their potential antigenicity by a variety of methods well known in the art. For example, a recombinant dog ZPC was modified by palmitylation was prepared as follows. Approximately 1 mg of recombinant ZPC produced using the plasmid pZ169 as described above was brought to a final concentration of 8M urea (total volume 0.2-0.3 mls.). A palmitylation solution (PI₂O/TEA) was then prepared by adding palmitic anhydride to triethylamine to give a final concentration of palmitic anhydride of 20 mg/ml of triethylamine.

Approximately 10 μ l of PI₂O/TEA solution was added to 1 mg of recombinant canine ZPC in 8M urea (described above). The mixture was allowed to stand at room temperature for a least two hours after which the preparation was ready for mixture with GMDP/oil adjuvant.

Chitosan modification is another useful modification of canine ZPC for the practice of the present invention. Briefly, 1.5 ml of sterile mineral oil was added to 1.5 ml of recombinant canine ZPC solution prepared as described above using the plasmid pZ169 (2 mg/ml ZPC, 3 mg total is 8M urea) was mixed with 5 drops of Arlacel A (mannide monooleate, Sigma, St, Louis, MO). Subsequently, 0.75 ml of Chitosan (2% wt/vol. is 0.5M sodium acetate, pH 5.0) was added, and the mixture was sonicated for 10-20 seconds, followed by the addition of 0.045 ml of 50% NaOH and another round of sonication for 10-20 seconds. Finally, 10 μ l of 10 mg/ml GMDP/8M urea was added.

A group of three dogs was immunized five times each at one-month intervals with subcutaneous injections of 1 mg doses of the N-terminal canine ZPC modified by the addition of chitosan prepared as described above. Immunized dogs developed antibody titers of 1:8000-1:16000 against heat solubilized dog zona pellucida (self-titers) using methods

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described above.⁶ The estrus cycle of the dogs showing self-titers was anovulatory and prolonged (4-6 weeks instead of the normal 10-day to 14-day cycle for normal dogs). Of the three immunized dogs, two have experienced their first estrus; one of the two dogs exhibited estrus six months after the first immunization and was bred and found to be infertile. The second of the two dogs experienced estrus and remained infertile nine months after the first immunization. The third dog has yet to experience estrus more than nine months after immunization.

Another group of four dogs were immunized three times at one-month intervals using 1 mg doses of palmitylated canine ZPC (prepared as described above) in GMDP/oil adjuvant administered subcutaneously. These animals achieved self-titers (against heat solubilized dog zona pellucida) of 1:4000-1:8000. Nearly seven months after immunization, two of the four dogs experienced estrus and remain infertile. The remaining two dogs have yet to experience estrus.

Another set of dogs was immunized 3 times at one-month intervals, using subcutaneous injections of 1 mg of recombinant canine ZPC produced using pZ166, (a plasmid similar to pZ169 but containing a DNA sequence encoding amino acids 23-379 of the canine ZPC protein) in GMDP/oil adjuvant. These animals failed to develop self-titers and became pregnant after breeding. Similarly, dogs immunized with canine ZPC fragments produced using the baculovirus system failed to induce infertility.

Example 19

Vaccination of Cows and Cats with Recombinant Zona Pellucida Proteins

Preliminary studies were undertaken to assess the ability of recombinant zona pellucida proteins to induce infertility in cows and cats.

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Cows were injected with 3 or more doses (in GMDP (250 μ g) oil adjuvant) of 1 mg of a variety of recombinantly derived ZPC proteins from canine and porcine sources including canine ZPC produced using the plasmid pZ169 as shown in Figure 5. Recombinant proteins were administered in an unmodified form and in palmitylated and chitosan modified forms. None of the ZP protein preparations induced self-titers or infertility in the vaccinated cows. Further studies are underway using different recombinant preparations of zona pellucida proteins and differing dosage regimens in attempts to induce self-titers and infertility in cows.

Similarly, cats were vaccinated with the following recombinant zona pellucida proteins: a mixture of recombinant feline ZPA, ZPB, and ZPC; porcine ZPC produced using pZ156 as described above and shown in Figure 3; and canine ZPC produced using the plasmid pZ169 described above and shown in Figure 5. Cats vaccinated using these ZP protein preparations produced antibody to the vaccine proteins, but produced no self-titers and were consequently fertile. Studies are ongoing to determine the effects of modifying the recombinant zona pellucida proteins in attempts to stimulate the production of self-titers and to induce infertility.

Studies are also ongoing to select other recombinantly derived zona pellucida protein fragments for testing as possible immunocontraceptives.

Numerous modifications in variations in the practice of the invention as illustrated in the above examples are expected to occur to those of ordinary skill in the art. Consequently, the illustrative examples are not intended to limit the scope of the invention as set out in the appended claims.

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SEQUENCE LISTING

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(ii) TITLE OF INVENTION: Materials and Methods for Immunocontraception

(iii) NUMBER OF SEQUENCES: 59

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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(C) CLASSIFICATION:

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(B) FILING DATE: 09-NOV-1992

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- 68 -

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2214 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Sus scrofa
 (D) DEVELOPMENTAL STAGE: Juvenile
 (E) HAPLOTYPE: Diploidy
 (F) TISSUE TYPE: Ovary
 (G) CELL TYPE: Oocyte

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 12..119

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 120..2153

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 12..2153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGG C AGG CAC AGA GGA GAC AGT GGG AGA CCC TTA AGC TGG CTC	50
Arg His Arg Gly Asp Ser Gly Arg Pro Leu Ser Trp Leu	
-36 -35 -30 -25	
AGT GCA AGC TGG AGG TCA CTT CTT CTA TTT TTC CCC CTT GTG ACT TCA	98
Ser Ala Ser Trp Arg Ser Leu Leu Leu Phe Phe Pro Leu Val Thr Ser	
-20 -15 -10	
GTG AAC TCC ATA GGT GTC AAT CAG TTG GTG AAT ACT GCC TTC CCA GGT	146
Val Asn Ser Ile Gly Val Asn Gln Leu Val Asn Thr Ala Phe Pro Gly	
-5 1 5	
ATT GTC ACT TGC CAT GAA AAT AGA ATG GTA GTG GAA TTT CCA AGA ATT	194
Ile Val Thr Cys His Glu Asn Arg Met Val Val Glu Phe Pro Arg Ile	
10 15 20 25	
CTT GGC ACT AAG ATA CAG TAC ACC TCT GTG GTG GAC CCT CTT GGT CTT	242
Leu Gly Thr Lys Ile Gln Tyr Thr Ser Val Val Asp Pro Leu Gly Leu	
30 35 40	
GAA ATG ATG AAC TGT ACT TAT GTT CTG GAC CCA GAA AAC CTC ACC CTG	290

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Glu Met Met Asn Cys Thr Tyr Val Leu Asp Pro Glu Asn Leu Thr Leu	
45 50 55	
AAG GCC CCA TAT GAA GCC TGT ACC AAA AGA GTG CGT GGC CAT CAC CAA	338
Lys Ala Pro Tyr Glu Ala Cys Thr Lys Arg Val Arg Gly His His Gln	
60 65 70	
ATG ACC ATC AGA CTC ATA GAT GAC AAT GCT GCT TTA AGA CAA GAG GCT	386
Met Thr Ile Arg Leu Ile Asp Asp Asn Ala Ala Leu Arg Gln Glu Ala	
75 80 85	
CTC ATG TAT CAC ATC AGC TGT CCT GTT ATG GGA GCA GAA GGC CCT GAT	434
Leu Met Tyr His Ile Ser Cys Pro Val Met Gly Ala Glu Gly Pro Asp	
90 95 100 105	
CAG CAT TCG GGA TCC ACA ATC TGC ATG AAA GAT TTC ATG TCT TTT ACC	482
Gln His Ser Gly Ser Thr Ile Cys Met Lys Asp Phe Met Ser Phe Thr	
110 115 120	
TTT AAC TTT TTT CCC GGG ATG GCT GAC GAA AAT GTG AAA CGT GAG GAT	530
Phe Asn Phe Phe Pro Gly Met Ala Asp Glu Asn Val Lys Arg Glu Asp	
125 130 135	
TCG AAG CAG CGC ATG GGA TGG AGC CTT GTA GTT GGT GAC GGT GAA AGA	578
Ser Lys Gln Arg Met Gly Trp Ser Leu Val Val Gly Asp Gly Glu Arg	
140 145 150	
GCC CGA ACT CTG ACC TTT CAG GAG GCC ATG ACC CAA GGA TAT AAT TTC	626
Ala Arg Thr Leu Thr Phe Gln Glu Ala Met Thr Gln Gly Tyr Asn Phe	
155 160 165	
CTG ATA GAG AAC CAG AAG ATG AAC ATC CAA GTG TCA TTC CAT GCC ACT	674
Leu Ile Glu Asn Gln Lys Met Asn Ile Gln Val Ser Phe His Ala Thr	
170 175 180 185	
GGA GTG ACT CGC TAC TCG CAA GGT AAC AGT CAT CTC TAC ATG GTA CCT	722
Gly Val Thr Arg Tyr Ser Gln Gly Asn Ser His Leu Tyr Met Val Pro	
190 195 200	
CTG AAG CTT AAA CAT GTA TCT CAT GGG CAG TCT CTC ATC TTA GCA TCA	770
Leu Lys Leu Lys His Val Ser His Gly Gln Ser Leu Ile Leu Ala Ser	
205 210 215	
CAA CTC ATC TGT GTG GCA GAT CCT GTG ACC TGT AAT GCC ACA CAC GTG	818
Gln Leu Ile Cys Val Ala Asp Pro Val Thr Cys Asn Ala Thr His Val	
220 225 230	
ACT CTT GCC ATA CCA GAG TTT CCT GGG AAG CTA AAA TCC GTG AAC TTG	866
Thr Leu Ala Ile Pro Glu Phe Pro Gly Lys Leu Lys Ser Val Asn Leu	
235 240 245	
GGA AGT GGG AAT ATT GCT GTG AGC CAG CTG CAC AAA CAC GGG ATT GAA	914
Gly Ser Gly Asn Ile Ala Val Ser Gln Leu His Lys His Gly Ile Glu	
250 255 260 265	
ATG GAA ACA ACA AAC GGC CTG AGG TTG CAT TTC AAC CAA ACT CTT CTC	962
Met Glu Thr Thr Asn Gly Leu Arg Leu His Phe Asn Gln Thr Leu Leu	
270 275 280	
AAA ACA AAT GTC TCT GAA AAA TGC CTA CCA CAT CAG TTG TAC TTA TCT	1010
Lys Thr Asn Val Ser Glu Lys Cys Leu Pro His Gln Leu Tyr Leu Ser	
285 290 295	
TCA CTC AAG CTG ACT TTT CAC AGT CAA CTA GAG GCA GTA TCC ATG GTG	1058
Ser Leu Lys Leu Thr Phe His Ser Gln Leu Glu Ala Val Ser Met Val	
300 305 310	

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ATT TAT CCT GAG TGT CTC TGT GAG TCA ACA GTC TCT TTA GTT TCA GAG Ile Tyr Pro Glu Cys Leu Cys Glu Ser Thr Val Ser Leu Val Ser Glu 315 320 325	1106
GAG CTA TGC ACT CAG GAT GGG TTT ATG GAC GTC AAG GTC CAC AGC CAC Glu Leu Cys Thr Gln Asp Gly Phe Met Asp Val Lys Val His Ser His 330 335 340 345	1154
CAA ACA AAA CCA GCT CTC AAC TTG GAT ACC CTC AGG GTG GGA GAC TCA Gln Thr Lys Pro Ala Leu Asn Leu Asp Thr Leu Arg Val Gly Asp Ser 350 355 360	1202
TCC TGC CAG CCA ACC TTT AAA GCT CCA GCT CAG GGG CTG GTA CAG TTT Ser Cys Gln Pro Thr Phe Lys Ala Pro Ala Gln Gly Leu Val Gln Phe 365 370 375	1250
CGC ATA CCC CTG AAT GGA TGT GGA ACA AGA CAT AAG TTC AAG AAT GAC Arg Ile Pro Leu Asn Gly Cys Gly Thr Arg His Lys Phe Lys Asn Asp 380 385 390	1298
AAA GTC ATC TAT GAA AAT GAA ATA CAT GCT CTC TGG GCA GAT CCT CCA Lys Val Ile Tyr Glu Asn Glu Ile His Ala Leu Trp Ala Asp Pro Pro 395 400 405	1346
AGC GCC GTT TCC AGA GAT AGT GAG TTC AGA ATG ACA GTG AGG TGC TCT Ser Ala Val Ser Arg Asp Ser Glu Phe Arg Met Thr Val Arg Cys Ser 410 415 420 425	1394
TAC AGC AGC AGC AAC ATG CTA ATA AAT ACC AAT GTT GAA AGT CTT CCT Tyr Ser Ser Ser Asn Met Leu Ile Asn Thr Asn Val Glu Ser Leu Pro 430 435 440	1442
TCT CCA GAG GCC TCA GTG AAG CCA GGT CCA CTT ACC CTG ACT CTG CAA Ser Pro Glu Ala Ser Val Lys Pro Gly Pro Leu Thr Leu Thr Leu Gln 445 450 455	1490
ACC TAC CCA GAT AAC GCC TAC CTG CAG CCT TAT GGG GAC AAG GAG TAC Thr Tyr Pro Asp Asn Ala Tyr Leu Gln Pro Tyr Gly Asp Lys Glu Tyr 460 465 470	1538
CCT GTG GTG AAA TAT CTC CGC CAA CCA ATT TAC CTA GAA GTG AGA ATC Pro Val Val Lys Tyr Leu Arg Gln Pro Ile Tyr Leu Glu Val Arg Ile 475 480 485	1586
CTC AAC AGG ACT GAC CCC AAC ATC AAG CTG GTC TTG GAT GAC TGC TGG Leu Asn Arg Thr Asp Pro Asn Ile Lys Leu Val Leu Asp Asp Cys Trp 490 495 500 505	1634
GCA ACA TCC ACA GAG GAC CCA GCC TCT CTC CCC CAG TGG AAT GTT GTC Ala Thr Ser Thr Glu Asp Pro Ala Ser Leu Pro Gln Trp Asn Val Val 510 515 520	1682
ATG GAT GGC TGT GAA TAC AAC CTG GAC AAC CAC AGA ACC ACC TTC CAT Met Asp Gly Cys Glu Tyr Asn Leu Asp Asn His Arg Thr Thr Phe His 525 530 535	1730
CCG GTG GGC TCC TCC GTG ACC TAT CCT AAC CAC CAT CAG AGG TTT GAT Pro Val Gly Ser Ser Val Thr Tyr Pro Asn His His Gln Arg Phe Asp 540 545 550	1778
GTG AAG ACC TTT GCC TTT GTG TCA GGG GCC CAA GGG GTC TCT CAA CTG Val Lys Thr Phe Ala Phe Val Ser Gly Ala Gln Gly Val Ser Gln Leu 555 560 565	1826
GTC TAC TTC CAC TGC AGT GTC TTC ATC TGC AAT CAA CTC TCT CCC ACC Val Tyr Phe His Cys Ser Val Phe Ile Cys Asn Gln Leu Ser Pro Thr 570 575 580 585	1874

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TTC TCT CTG TGT TCT GTG ACT TGC CAT GGG CCA TCT AGG AGC CGG CGA 1922
 Phe Ser Leu Cys Ser Val Thr Cys His Gly Pro Ser Arg Ser Arg Arg
 590 595 600
 GCT ACA GGG ACC ACT GAG GAA GAG AAA ATG ATA GTG AGT CTC CCG GGC 1970
 Ala Thr Gly Thr Thr Glu Glu Glu Lys Met Ile Val Ser Leu Pro Gly
 605 610 615
 CCC ATC CTG CTG TTG TCA GAT GGC TCT TCA CTC AGA GAT GCT GTG AAC 2018
 Pro Ile Leu Leu Leu Ser Asp Gly Ser Ser Leu Arg Asp Ala Val Asn
 620 625 630
 TCT AAA GGA TCC AGA ACC AAC GGA TAT GTT GCT TTT AAA ACT ATG GTT 2066
 Ser Lys Gly Ser Arg Thr Asn Gly Tyr Val Ala Phe Lys Thr Met Val
 635 640 645
 GCT ATG GTT GCT TCA GCA GGC ATC GTG GCA ACT CTA GGC CTC ATC AGC 2114
 Ala Met Val Ala Ser Ala Gly Ile Val Ala Thr Leu Gly Leu Ile Ser
 650 655 660 665
 TAC CTG CAC AAA AAA AGA ATC ATG ATG TTA AAT CAC TAATTTGGAT 2160
 Tyr Leu His Lys Lys Arg Ile Met Met Leu Asn His
 670 675
 TTTCAAATAA AAGTGAAGT AAGCCTCTTC TAAAAA AAAAACC GGA ATTC 2214

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Arg His Arg Gly Asp Ser Gly Arg Pro Leu Ser Trp Leu Ser Ala Ser
 -36 -35 -30 -25
 Trp Arg Ser Leu Leu Leu Phe Phe Pro Leu Val Thr Ser Val Asn Ser
 -20 -15 -10 -5
 Ile Gly Val Asn Gln Leu Val Asn Thr Ala Phe Pro Gly Ile Val Thr
 1 5 10
 Cys His Glu Asn Arg Met Val Val Glu Phe Pro Arg Ile Leu Gly Thr
 15 20 25
 Lys Ile Gln Tyr Thr Ser Val Val Asp Pro Leu Gly Leu Glu Met Met
 30 35 40
 Asn Cys Thr Tyr Val Leu Asp Pro Glu Asn Leu Thr Leu Lys Ala Pro
 45 50 55 60
 Tyr Glu Ala Cys Thr Lys Arg Val Arg Gly His His Gln Met Thr Ile
 65 70 75
 Arg Leu Ile Asp Asp Asn Ala Ala Leu Arg Gln Glu Ala Leu Met Tyr
 80 85 90
 His Ile Ser Cys Pro Val Met Gly Ala Glu Gly Pro Asp Gln His Ser
 95 100 105
 Gly Ser Thr Ile Cys Met Lys Asp Phe Met Ser Phe Thr Phe Asn Phe
 110 115 120

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Phe Pro Gly Met Ala Asp Glu Asn Val Lys Arg Glu Asp Ser Lys Gln
 125 130 135 140
 Arg Met Gly Trp Ser Leu Val Val Gly Asp Gly Glu Arg Ala Arg Thr
 145 150 155
 Leu Thr Phe Gln Glu Ala Met Thr Gln Gly Tyr Asn Phe Leu Ile Glu
 160 165 170
 Asn Gln Lys Met Asn Ile Gln Val Ser Phe His Ala Thr Gly Val Thr
 175 180 185
 Arg Tyr Ser Gln Gly Asn Ser His Leu Tyr Met Val Pro Leu Lys Leu
 190 195 200
 Lys His Val Ser His Gly Gln Ser Leu Ile Leu Ala Ser Gln Leu Ile
 205 210 215 220
 Cys Val Ala Asp Pro Val Thr Cys Asn Ala Thr His Val Thr Leu Ala
 225 230 235
 Ile Pro Glu Phe Pro Gly Lys Leu Lys Ser Val Asn Leu Gly Ser Gly
 240 245 250
 Asn Ile Ala Val Ser Gln Leu His Lys His Gly Ile Glu Met Glu Thr
 255 260 265
 Thr Asn Gly Leu Arg Leu His Phe Asn Gln Thr Leu Leu Lys Thr Asn
 270 275 280
 Val Ser Glu Lys Cys Leu Pro His Gln Leu Tyr Leu Ser Ser Leu Lys
 285 290 295 300
 Leu Thr Phe His Ser Gln Leu Glu Ala Val Ser Met Val Ile Tyr Pro
 305 310 315
 Glu Cys Leu Cys Glu Ser Thr Val Ser Leu Val Ser Glu Glu Leu Cys
 320 325 330
 Thr Gln Asp Gly Phe Met Asp Val Lys Val His Ser His Gln Thr Lys
 335 340 345
 Pro Ala Leu Asn Leu Asp Thr Leu Arg Val Gly Asp Ser Ser Cys Gln
 350 355 360
 Pro Thr Phe Lys Ala Pro Ala Gln Gly Leu Val Gln Phe Arg Ile Pro
 365 370 375 380
 Leu Asn Gly Cys Gly Thr Arg His Lys Phe Lys Asn Asp Lys Val Ile
 385 390 395
 Tyr Glu Asn Glu Ile His Ala Leu Trp Ala Asp Pro Pro Ser Ala Val
 400 405 410
 Ser Arg Asp Ser Glu Phe Arg Met Thr Val Arg Cys Ser Tyr Ser Ser
 415 420 425
 Ser Asn Met Leu Ile Asn Thr Asn Val Glu Ser Leu Pro Ser Pro Glu
 430 435 440
 Ala Ser Val Lys Pro Gly Pro Leu Thr Leu Thr Leu Gln Thr Tyr Pro
 445 450 455 460
 Asp Asn Ala Tyr Leu Gln Pro Tyr Gly Asp Lys Glu Tyr Pro Val Val
 465 470 475
 Lys Tyr Leu Arg Gln Pro Ile Tyr Leu Glu Val Arg Ile Leu Asn Arg

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480	485	490
Thr Asp Pro Asn Ile Lys Leu Val	Leu Asp Asp Cys Trp Ala Thr Ser	
495	500	505
Thr Glu Asp Pro Ala Ser Leu Pro Gln Trp Asn Val Val Met Asp Gly		
510	515	520
Cys Glu Tyr Asn Leu Asp Asn His Arg Thr Thr Phe His Pro Val Gly		
525	530	535
Ser Ser Val Thr Tyr Pro Asn His His Gln Arg Phe Asp Val Lys Thr		
545	550	555
Phe Ala Phe Val Ser Gly Ala Gln Gly Val Ser Gln Leu Val Tyr Phe		
560	565	570
His Cys Ser Val Phe Ile Cys Asn Gln Leu Ser Pro Thr Phe Ser Leu		
575	580	585
Cys Ser Val Thr Cys His Gly Pro Ser Arg Ser Arg Arg Ala Thr Gly		
590	595	600
Thr Thr Glu Glu Glu Lys Met Ile Val Ser Leu Pro Gly Pro Ile Leu		
605	610	615
Leu Leu Ser Asp Gly Ser Ser Leu Arg Asp Ala Val Asn Ser Lys Gly		
625	630	635
Ser Arg Thr Asn Gly Tyr Val Ala Phe Lys Thr Met Val Ala Met Val		
640	645	650
Ala Ser Ala Gly Ile Val Ala Thr Leu Gly Leu Ile Ser Tyr Leu His		
655	660	665
Lys Lys Arg Ile Met Met Leu Asn His		
670	675	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Sus scrofa
- (D) DEVELOPMENTAL STAGE: Juvenile
- (E) HAPLOTYPE: Diploidy
- (F) TISSUE TYPE: Ovary
- (G) CELL TYPE: Oocyte

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 38..445

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 446..1648

(ix) FEATURE:

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(A) NAME/KEY: CDS
(B) LOCATION: 38..1648

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGG TGAAGTACC TGTCTCCGC AGGCGCT ATG TGG TTG CGG CCG TCC	55
Met Trp Leu Arg Pro Ser	
-136-135	
ATC TGG CTC TGC TTT CCG CTG TGT CTT GCT CTG CCA GGC CAG TCT CAG	103
Ile Trp Leu Cys Phe Pro Leu Cys Leu Ala Leu Pro Gly Gln Ser Gln	
-130 -125 -120 -115	
CCC AAA GCA GCA GAT GAC CTT GGT GGC CTC TAC TGT GGG CCA AGC AGC	151
Pro Lys Ala Ala Asp Asp Leu Gly Gly Leu Tyr Cys Gly Pro Ser Ser	
-110 -105 -100	
TTT CAT TTC TCC ATA AAT CTT CTC AGC CAG GAC ACA GCA ACT CCT CCT	199
Phe His Phe Ser Ile Asn Leu Leu Ser Gln Asp Thr Ala Thr Pro Pro	
-95 -90 -85	
GCA CTG GTG GTT TGG GAC AGG CGC GGG CGG CTG CAC AAG CTG CAG AAT	247
Ala Leu Val Val Trp Asp Arg Arg Gly Arg Leu His Lys Leu Gln Asn	
-80 -75 -70	
GAC TCT GGC TGT GGC ACG TGG GTC CAC AAG GGC CCA GGC AGC TCC ATG	295
Asp Ser Gly Cys Gly Thr Trp Val His Lys Gly Pro Gly Ser Ser Met	
-65 -60 -55	
GGA GTG GAA GCA TCC TAC AGA GGC TGC TAT GTG ACT GAG TGG GAC TCT	343
Gly Val Glu Ala Ser Tyr Arg Gly Cys Tyr Val Thr Glu Trp Asp Ser	
-50 -45 -40 -35	
CAC TAC CTC ATG CCC ATT GGA CTT GAA GAA GCA GAT GCA GGT GGA CAC	391
His Tyr Leu Met Pro Ile Gly Leu Glu Glu Ala Asp Ala Gly Gly His	
-30 -25 -20	
AGA ACA GTC ACA GAG ACG AAA CTG TTT AAG TGC CCT GTG GAT TTC CTA	439
Arg Thr Val Thr Glu Thr Lys Leu Phe Lys Cys Pro Val Asp Phe Leu	
-15 -10 -5	
GCT CTT GAT GTT CCA ACC ATT GGC CTT TGT GAT GCT GTC CCA GTG TGG	487
Ala Leu Asp Val Pro Thr Ile Gly Leu Cys Asp Ala Val Pro Val Trp	
1 5 10	
GAC CGA TTG CCA TGT GCT CCT CCA CCC ATC ACT CAA GGA GAA TGC AAG	535
Asp Arg Leu Pro Cys Ala Pro Pro Pro Ile Thr Gln Gly Glu Cys Lys	
15 20 25 30	
CAG CTT GGC TGC TGC TAC AAC TCG GAA GAG GTC CCT TCT TGT TAC TAT	583
Gln Leu Gly Cys Cys Tyr Asn Ser Glu Glu Val Pro Ser Cys Tyr Tyr	
35 40 45	
GGA AAC ACA GTG ACC TCA CGC TGT ACC CAA GAT GGC CAC TTC TCC ATC	631
Gly Asn Thr Val Thr Ser Arg Cys Thr Gln Asp Gly His Phe Ser Ile	
50 55 60	
GCT GTG TCT CGC AAT GTG ACC TCA CCT CCA CTG CTC TGG GAT TCT GTG	679
Ala Val Ser Arg Asn Val Thr Ser Pro Pro Leu Leu Trp Asp Ser Val	
65 70 75	
CAC CTG GCC TTC AGA AAT GAC AGT GAA TGT AAA CCT GTG ATG GAA ACA	727
His Leu Ala Phe Arg Asn Asp Ser Glu Cys Lys Pro Val Met Glu Thr	
80 85 90	
CAC ACT TTT GTC CTC TTC CGG TTT CCA TTT AGT TCC TGT GGG ACT GCA	775

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His Thr Phe Val Leu Phe Arg Phe Pro Phe Ser Ser Cys Gly Thr Ala	
95 100 105 110	
AAA CGG GTA ACT GGG AAC CAG GCG GTA TAT GAA AAT GAG CTG GTA GCA	823
Lys Arg Val Thr Gly Asn Gln Ala Val Tyr Glu Asn Glu Leu Val Ala	
115 120 125	
GCT CGG GAT GTG AGG ACT TGG AGC CAT GGT TCT ATT ACC CGA GAC AGC	871
Ala Arg Asp Val Arg Thr Trp Ser His Gly Ser Ile Thr Arg Asp Ser	
130 135 140	
ATC TTC AGG CTT CGA GTC AGT TGT ATC TAC TCT GTA AGT AGC AGT GCT	919
Ile Phe Arg Leu Arg Val Ser Cys Ile Tyr Ser Val Ser Ser Ser Ala	
145 150 155	
CTC CCA GTT AAC ATC CAG GTT TTC ACT CTC CCA CCA CCG CTT CCG GAG	967
Leu Pro Val Asn Ile Gln Val Phe Thr Leu Pro Pro Pro Leu Pro Glu	
160 165 170	
ACC CAC CCT GGA CCT CTT ACT CTG GAG CTT CAG ATT GCC AAA GAT GAA	1015
Thr His Pro Gly Pro Leu Thr Leu Glu Leu Gln Ile Ala Lys Asp Glu	
175 180 185 190	
CGC TAT GGC TCC TAC TAC AAT GCT AGT GAC TAC CCG GTG GTG AAA TTG	1063
Arg Tyr Gly Ser Tyr Tyr Asn Ala Ser Asp Tyr Pro Val Val Lys Leu	
195 200 205	
CTT CGG GAG CCC ATC TAT GTG GAG GTC TCT ATC CGT CAC CGA ACA GAC	1111
Leu Arg Glu Pro Ile Tyr Val Glu Val Ser Ile Arg His Arg Thr Asp	
210 215 220	
CCC AGT CTC GGG CTG CAC CTG CAC CAG TGC TGG GCC ACA CCC GGC ATG	1159
Pro Ser Leu Gly Leu His Leu His Gln Cys Trp Ala Thr Pro Gly Met	
225 230 235	
AGC CCC CTG CTC CAG CCA CAG TGG CCC ATG CTA GTC AAT GGA TGC CCC	1207
Ser Pro Leu Leu Gln Pro Gln Trp Pro Met Leu Val Asn Gly Cys Pro	
240 245 250	
TAC ACT GGA GAC AAC TAC CAG ACC AAA CTG ATC CCT GTC CAG AAA GCC	1255
Tyr Thr Gly Asp Asn Tyr Gln Thr Lys Leu Ile Pro Val Gln Lys Ala	
255 260 265 270	
TCA AAC CTG CTA TTT CCT TCT CAC TAC CAG CGT TTC AGT GTT TCC ACC	1303
Ser Asn Leu Leu Phe Pro Ser His Tyr Gln Arg Phe Ser Val Ser Thr	
275 280 285	
TTC AGT TTT GTG GAC TCT GTG GCA AAG CAG GCA CTC AAG GGA CCG GTG	1351
Phe Ser Phe Val Asp Ser Val Ala Lys Gln Ala Leu Lys Gly Pro Val	
290 295 300	
TAT CTG CAT TGT ACT GCA TCG GTC TGC AAG CCT GCA GGG GCA CCG ATC	1399
Tyr Leu His Cys Thr Ala Ser Val Cys Lys Pro Ala Gly Ala Pro Ile	
305 310 315	
TGT GTG ACA ACC TGT CCT GCT GCC AGA CGA AGA AGA AGT TCT GAC ATC	1447
Cys Val Thr Thr Cys Pro Ala Ala Arg Arg Arg Ser Ser Asp Ile	
320 325 330	
CAT TTT CAG AAT GGC ACT GCT AGC ATT TCT AGC AAG GGT CCC ATG ATT	1495
His Phe Gln Asn Gly Thr Ala Ser Ile Ser Ser Lys Gly Pro Met Ile	
335 340 345 350	
CTA CTC CAA GCC ACT CGG GAC TCT TCA GAA AGG CTC CAT AAA TAC TCA	1543
Leu Leu Gln Ala Thr Arg Asp Ser Ser Glu Arg Leu His Lys Tyr Ser	
355 360 365	

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AGG CCT CCT GTA GAC TCC CAT GCT CTG TGG GTG GCT GGC CTC TTG GGA 1591
 Arg Pro Pro Val Asp Ser His Ala Leu Trp Val Ala Gly Leu Leu Gly
 370 375 380
 AGC TTA ATT ATT GGA GCC TTT TTA GTG TCC TAC CTG GTC TTC AGG AAA 1639
 Ser Leu Ile Ile Gly Ala Leu Leu Val Ser Tyr Leu Val Phe Arg Lys
 385 390 395
 TGG AGA TGAGTTACTC AGACCAAATG TGCAATAAA ACCAATAAAA CAAAACCGGA 1695
 Trp Arg
 400
 ATTC 1699

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 536 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Trp Leu Arg Pro Ser Ile Trp Leu Cys Phe Pro Leu Cys Leu Ala
 -136 -135 -130 -125
 Leu Pro Gly Gln Ser Gln Pro Lys Ala Ala Asp Asp Leu Gly Gly Leu
 -120 -115 -110 -105
 Tyr Cys Gly Pro Ser Ser Phe His Phe Ser Ile Asn Leu Leu Ser Gln
 -100 -95 -90
 Asp Thr Ala Thr Pro Pro Ala Leu Val Val Trp Asp Arg Arg Gly Arg
 -85 -80 -75
 Leu His Lys Leu Gln Asn Asp Ser Gly Cys Gly Thr Trp Val His Lys
 -70 -65 -60
 Gly Pro Gly Ser Ser Met Gly Val Glu Ala Ser Tyr Arg Gly Cys Tyr
 -55 -50 -45
 Val Thr Glu Trp Asp Ser His Tyr Leu Met Pro Ile Gly Leu Glu Glu
 -40 -35 -30 -25
 Ala Asp Ala Gly Gly His Arg Thr Val Thr Glu Thr Lys Leu Phe Lys
 -20 -15 -10
 Cys Pro Val Asp Phe Leu Ala Leu Asp Val Pro Thr Ile Gly Leu Cys
 -5 1 5
 Asp Ala Val Pro Val Trp Asp Arg Leu Pro Cys Ala Pro Pro Pro Ile
 10 15 20
 Thr Gln Gly Glu Cys Lys Gln Leu Gly Cys Cys Tyr Asn Ser Glu Glu
 25 30 35 40
 Val Pro Ser Cys Tyr Tyr Gly Asn Thr Val Thr Ser Arg Cys Thr Gln
 45 50 55
 Asp Gly His Phe Ser Ile Ala Val Ser Arg Asn Val Thr Ser Pro Pro
 60 65 70
 Leu Leu Trp Asp Ser Val His Leu Ala Phe Arg Asn Asp Ser Glu Cys

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75					80					85					
Lys	Pro	Val	Met	Glu	Thr	His	Thr	Phe	Val	Leu	Phe	Arg	Phe	Pro	Phe
90					95					100					
Ser	Ser	Cys	Gly	Thr	Ala	Lys	Arg	Val	Thr	Gly	Asn	Gln	Ala	Val	Tyr
105					110					115					120
Glu	Asn	Glu	Leu	Val	Ala	Ala	Arg	Asp	Val	Arg	Thr	Trp	Ser	His	Gly
			125						130					135	
Ser	Ile	Thr	Arg	Asp	Ser	Ile	Phe	Arg	Leu	Arg	Val	Ser	Cys	Ile	Tyr
			140					145					150		
Ser	Val	Ser	Ser	Ser	Ala	Leu	Pro	Val	Asn	Ile	Gln	Val	Phe	Thr	Leu
			155				160						165		
Pro	Pro	Pro	Leu	Pro	Glu	Thr	His	Pro	Gly	Pro	Leu	Thr	Leu	Glu	Leu
	170					175					180				
Gln	Ile	Ala	Lys	Asp	Glu	Arg	Tyr	Gly	Ser	Tyr	Tyr	Asn	Ala	Ser	Asp
185					190					195					200
Tyr	Pro	Val	Val	Lys	Leu	Leu	Arg	Glu	Pro	Ile	Tyr	Val	Glu	Val	Ser
				205					210					215	
Ile	Arg	His	Arg	Thr	Asp	Pro	Ser	Leu	Gly	Leu	His	Leu	His	Gln	Cys
			220					225					230		
Trp	Ala	Thr	Pro	Gly	Met	Ser	Pro	Leu	Leu	Gln	Pro	Gln	Trp	Pro	Met
			235				240					245			
Leu	Val	Asn	Gly	Cys	Pro	Tyr	Thr	Gly	Asp	Asn	Tyr	Gln	Thr	Lys	Leu
	250					255					260				
Ile	Pro	Val	Gln	Lys	Ala	Ser	Asn	Leu	Leu	Phe	Pro	Ser	His	Tyr	Gln
265					270					275					280
Arg	Phe	Ser	Val	Ser	Thr	Phe	Ser	Phe	Val	Asp	Ser	Val	Ala	Lys	Gln
				285					290					295	
Ala	Leu	Lys	Gly	Pro	Val	Tyr	Leu	His	Cys	Thr	Ala	Ser	Val	Cys	Lys
			300					305					310		
Pro	Ala	Gly	Ala	Pro	Ile	Cys	Val	Thr	Thr	Cys	Pro	Ala	Ala	Arg	Arg
			315				320					325			
Arg	Arg	Ser	Ser	Asp	Ile	His	Phe	Gln	Asn	Gly	Thr	Ala	Ser	Ile	Ser
	330					335					340				
Ser	Lys	Gly	Pro	Met	Ile	Leu	Leu	Gln	Ala	Thr	Arg	Asp	Ser	Ser	Glu
345					350					355					360
Arg	Leu	His	Lys	Tyr	Ser	Arg	Pro	Pro	Val	Asp	Ser	His	Ala	Leu	Trp
				365					370					375	
Val	Ala	Gly	Leu	Leu	Gly	Ser	Leu	Ile	Ile	Gly	Ala	Leu	Leu	Val	Ser
			380					385					390		
Tyr	Leu	Val	Phe	Arg	Lys	Trp	Arg								
			395				400								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1326 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Sus scrofa
 (D) DEVELOPMENTAL STAGE: Juvenile
 (E) HAPLOTYPE: Diploidy
 (F) TISSUE TYPE: Ovary
 (G) CELL TYPE: Oocyte

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 25..105

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 106..1290

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 25..1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGG GCCTGTGAG TGCC ATG GCG CCG AGC TGG AGG TTC TTC GTC	51
Met Ala Pro Ser Trp Arg Phe Phe Val	
-27 -25 -20	
TGC TTT CTG CTC TGG GGA GGT ACA GAG CTA TGC AGC CCG CAG CCC GTC	99
Cys Phe Leu Leu Trp Gly Gly Thr Glu Leu Cys Ser Pro Gln Pro Val	
-15 -10 -5	
TGG CAG GAC GAA GGC CAG CGC TTG AGG CCC TCA AAG CCA CCC ACC GTA	147
Trp Gln Asp Glu Gly Gln Arg Leu Arg Pro Ser Lys Pro Pro Thr Val	
1 5 10	
ATG GTG GAG TGT CAG GAG GCC CAG CTG GTG GTC ATT GTC AGC AAA GAC	195
Met Val Glu Cys Gln Glu Ala Gln Leu Val Val Ile Val Ser Lys Asp	
15 20 25 30	
CTT TTC GGT ACC GGG AAG CTC ATC AGG CCT GCA GAT CTC AGC CTG GGC	243
Leu Phe Gly Thr Gly Lys Leu Ile Arg Pro Ala Asp Leu Ser Leu Gly	
35 40 45	
CCT GCA AAG TGT GAG CCG CTG GTC TCT CAG GAC ACG GAC GCA GTG GTC	291
Pro Ala Lys Cys Glu Pro Leu Val Ser Gln Asp Thr Asp Ala Val Val	
50 55 60	
AGG TTT GAG GTT GGG CTG CAC GAG TGT GGC AGC AGC TTG CAG GTG ACT	339
Arg Phe Glu Val Gly Leu His Glu Cys Gly Ser Ser Leu Gln Val Thr	
65 70 75	
GAT GAT GCT CTG GTG TAC AGC ACC TTC CTG CGC CAT GAC CCC CGC CCT	387
Asp Asp Ala Leu Val Tyr Ser Thr Phe Leu Arg His Asp Pro Arg Pro	
80 85 90	
GCA GGA AAC CTG TCC ATC CTG AGG ACG AAC CGT GCG GAG GTC CCC ATC	435
Ala Gly Asn Leu Ser Ile Leu Arg Thr Asn Arg Ala Glu Val Pro Ile	
95 100 105 110	

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GAG TGT CAC TAC CCC AGG CAG GGC AAC GTG AGC AGC TGG GCC ATC CTG Glu Cys His Tyr Pro Arg Gln Gly Asn Val Ser Ser Trp Ala Ile Leu 115 120 125	483
CCC ACC TGG GTG CCC TTC AGG ACC ACG GTG TTC TCC GAG GAG AAG CTG Pro Thr Trp Val Pro Phe Arg Thr Thr Val Phe Ser Glu Lys Leu 130 135 140	531
GTG TTC TCT CTG CGC CTG ATG GAG GAA AAC TGG AGT GCC GAG AAG ATG Val Phe Ser Leu Arg Leu Met Glu Glu Asn Trp Ser Ala Glu Lys Met 145 150 155	579
ACG CCC ACC TTC CAG CTG GGG GAC AGA GCC CAC CTC CAG GCC CAA GTC Thr Pro Thr Phe Gln Leu Gly Asp Arg Ala His Leu Gln Ala Gln Val 160 165 170	627
CAC ACC GGC AGC CAC GTG CCA CTG AGG CTG TTT GTG GAC CAC TGT GTG His Thr Gly Ser His Val Pro Leu Arg Leu Phe Val Asp His Cys Val 175 180 185 190	675
GCC ACG CTG ACG CCG GAC TGG AAC ACC TCC CCC TCT CAC ACC ATC GTG Ala Thr Leu Thr Pro Asp Trp Asn Thr Ser Pro Ser His Thr Ile Val 195 200 205	723
GAC TTC CAC GGC TGT CTC GTG GAC GGT CTC ACT GAG GCC TCA TCT GCT Asp Phe His Gly Cys Leu Val Asp Gly Leu Thr Glu Ala Ser Ser Ala 210 215 220	771
TTC AAA GCA CCT AGA CCT GGA CCA GAG ACG CTC CAG TTC ACC GTG GAT Phe Lys Ala Pro Arg Pro Gly Pro Glu Thr Leu Gln Phe Thr Val Asp 225 230 235	819
GTG TTC CAT TTT GCT AAT GAT TCC AGA AAC ACG ATC TAC ATC ACC TGC Val Phe His Phe Ala Asn Asp Ser Arg Asn Thr Ile Tyr Ile Thr Cys 240 245 250	867
CAT CTG AAG GTC ACT CCG GCT GAC CGA GTC CCG GAC CAA CTC AAC AAA His Leu Lys Val Thr Pro Ala Asp Arg Val Pro Asp Gln Leu Asn Lys 255 260 265 270	915
GCC TGT TCC TTC AGC AAG TCC TCC AAC AGG TGG TCC CCG GTG GAA GGG Ala Cys Ser Phe Ser Lys Ser Ser Asn Arg Trp Ser Pro Val Glu Gly 275 280 285	963
CCT GCT GTT ATC TGT CGT TGC TGT CAC AAG GGG CAG TGT GGT ACC CCA Pro Ala Val Ile Cys Arg Cys Cys His Lys Gly Gln Cys Gly Thr Pro 290 295 300	1011
AGC CTT TCC AGG AAG CTG TCT ATG CCG AAG AGA CAG TCT GCT CCC CGC Ser Leu Ser Arg Lys Leu Ser Met Pro Lys Arg Gln Ser Ala Pro Arg 305 310 315	1059
AGT CGC AGG CAC GTG ACA GAT GAA GCA GAT GTC ACA GTG GGG CCT CTG Ser Arg Arg His Val Thr Asp Glu Ala Asp Val Thr Val Gly Pro Leu 320 325 330	1107
ATC TTC CTG GGC AAG ACG AGT GAC CAC GGT GTG GAA GGG TCC ACC TCC Ile Phe Leu Gly Lys Thr Ser Asp His Gly Val Glu Gly Ser Thr Ser 335 340 345 350	1155
TCC CCC ACC TCG GTG ATG GTG GGC TTG GGC CTG GCC ACC GTG GTG ACC Ser Pro Thr Ser Val Met Val Gly Leu Gly Leu Ala Thr Val Val Thr 355 360 365	1203
TTG ACT CTG GCT ACC ATT GTC CTG GGT GTG CCC AGG AGG CGT CGG GCT Leu Thr Leu Ala Thr Ile Val Leu Gly Val Pro Arg Arg Arg Arg Ala	1251

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370 375 380
 GCT GCC CAC CTT GTG TGC CCC GTG TCT GCT TCC CAA TAAAAGGAGA 1297
 Ala Ala His Leu Val Cys Pro Val Ser Ala Ser Gln
 385 390
 AACATGAAAA AAAAAAAAAA CCGGAATTC 1326

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Pro Ser Trp Arg Phe Phe Val Cys Phe Leu Leu Trp Gly Gly
 -27 -25 -20 -15
 Thr Glu Leu Cys Ser Pro Gln Pro Val Trp Gln Asp Glu Gly Gln Arg
 -10 -5 1 5
 Leu Arg Pro Ser Lys Pro Pro Thr Val Met Val Glu Cys Gln Glu Ala
 10 15 20
 Gln Leu Val Val Ile Val Ser Lys Asp Leu Phe Gly Thr Gly Lys Leu
 25 30 35
 Ile Arg Pro Ala Asp Leu Ser Leu Gly Pro Ala Lys Cys Glu Pro Leu
 40 45 50
 Val Ser Gln Asp Thr Asp Ala Val Val Arg Phe Glu Val Gly Leu His
 55 60 65
 Glu Cys Gly Ser Ser Leu Gln Val Thr Asp Asp Ala Leu Val Tyr Ser
 70 75 80 85
 Thr Phe Leu Arg His Asp Pro Arg Pro Ala Gly Asn Leu Ser Ile Leu
 90 95 100
 Arg Thr Asn Arg Ala Glu Val Pro Ile Glu Cys His Tyr Pro Arg Gln
 105 110 115
 Gly Asn Val Ser Ser Trp Ala Ile Leu Pro Thr Trp Val Pro Phe Arg
 120 125 130
 Thr Thr Val Phe Ser Glu Glu Lys Leu Val Phe Ser Leu Arg Leu Met
 135 140 145
 Glu Glu Asn Trp Ser Ala Glu Lys Met Thr Pro Thr Phe Gln Leu Gly
 150 155 160 165
 Asp Arg Ala His Leu Gln Ala Gln Val His Thr Gly Ser His Val Pro
 170 175 180
 Leu Arg Leu Phe Val Asp His Cys Val Ala Thr Leu Thr Pro Asp Trp
 185 190 195
 Asn Thr Ser Pro Ser His Thr Ile Val Asp Phe His Gly Cys Leu Val
 200 205 210
 Asp Gly Leu Thr Glu Ala Ser Ser Ala Phe Lys Ala Pro Arg Pro Gly
 215 220 225

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Pro Glu Thr Leu Gln Phe Thr Val Asp Val Phe His Phe Ala Asn Asp
 230 235 240 245
 Ser Arg Asn Thr Ile Tyr Ile Thr Cys His Leu Lys Val Thr Pro Ala
 250 255 260
 Asp Arg Val Pro Asp Gln Leu Asn Lys Ala Cys Ser Phe Ser Lys Ser
 265 270 275
 Ser Asn Arg Trp Ser Pro Val Glu Gly Pro Ala Val Ile Cys Arg Cys
 280 285 290
 Cys His Lys Gly Gln Cys Gly Thr Pro Ser Leu Ser Arg Lys Leu Ser
 295 300 305
 Met Pro Lys Arg Gln Ser Ala Pro Arg Ser Arg Arg His Val Thr Asp
 310 315 320 325
 Glu Ala Asp Val Thr Val Gly Pro Leu Ile Phe Leu Gly Lys Thr Ser
 330 335 340
 Asp His Gly Val Glu Gly Ser Thr Ser Ser Pro Thr Ser Val Met Val
 345 350 355
 Gly Leu Gly Leu Ala Thr Val Val Thr Leu Thr Leu Ala Thr Ile Val
 360 365 370
 Leu Gly Val Pro Arg Arg Arg Arg Ala Ala Ala His Leu Val Cys Pro
 375 380 385
 Val Ser Ala Ser Gln
 390

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Oryctolagus cuniculus*
- (D) DEVELOPMENTAL STAGE: Juvenile
- (E) HAPLOTYPE: Diploidy
- (F) TISSUE TYPE: Ovary
- (G) CELL TYPE: Oocyte

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 17..1261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGCGG CCGGCC TAC GGG CTC TTC GTT TGC CTA CTG CTC TGG GGA
 Tyr Gly Leu Phe Val Cys Leu Leu Leu Trp Gly
 1 5 10

49

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GGC TCG GAG CTG TGC TGC CCC CAG CCG CTC TGG TTC TGG CAG GGC GGG Gly Ser Glu Leu Cys Cys Pro Gln Pro Leu Trp Phe Trp Gln Gly Gly	97
15 20 25	
ACC CGC CAG CCC GCG CCC TCC GTG ACG CCC GTG GTG GTG GAG TGT CTG Thr Arg Gln Pro Ala Pro Ser Val Thr Pro Val Val Glu Cys Leu	145
30 35 40	
GAG GCC CCG CTC GTG GTC ACG GTC AGC AGG GAC CTT TTT GGC ACC GGG Glu Ala Arg Leu Val Val Thr Ser Arg Asp Leu Phe Gly Thr Gly	193
45 50 55	
AAG CTC ATC CAG GAG GCC GAC CTC AGC CTG GGC CCC GAG GGC TGC GAG Lys Leu Ile Gln Glu Ala Asp Leu Ser Leu Gly Pro Glu Gly Cys Glu	241
60 65 70 75	
CCC CAG GCC TCC ACG GAC GCC GTG GTC AGG TTC GAG GTC GGG CTG CAT Pro Gln Ala Ser Thr Asp Ala Val Val Arg Phe Glu Val Gly Leu His	289
80 85 90	
GAA TGT GGT AAC AGC GTG CAG GTG ACT GAC GAC TCC CTG GTG TAC AGC Glu Cys Gly Asn Ser Val Gln Val Thr Asp Asp Ser Leu Val Tyr Ser	337
95 100 105	
TCC TTC CTG CTC CAC GAC CCC CGC CCC GCG GGA AAC CTG TCC ATC CTC Ser Phe Leu Leu His Asp Pro Arg Pro Ala Gly Asn Leu Ser Ile Leu	385
110 115 120	
AGG ACC AAC CGC GCC GAG GTC CCC ATC GAG TGC CGC TAC CCC AGG CAG Arg Thr Asn Arg Ala Glu Val Pro Ile Glu Cys Arg Tyr Pro Arg Gln	433
125 130 135	
GGC AAC GTG AGC AGC CCG GCG ATC CTG CCG ACC TGG GTG CCC TTC TGG Gly Asn Val Ser Ser Arg Ala Ile Leu Pro Thr Trp Val Pro Phe Trp	481
140 145 150 155	
ACC ACG GTA CTG TCA GAG GAG AGG CTG GTG TTC TCC CTG CGC CTC ATG Thr Thr Val Leu Ser Glu Glu Arg Leu Val Phe Ser Leu Arg Leu Met	529
160 165 170	
GAG GAG AAC TGG AGC CGA GAA AAG ATG TCC CCC ACC TTC CAC CTG GGC Glu Glu Asn Trp Ser Arg Glu Lys Met Ser Pro Thr Phe His Leu Gly	577
175 180 185	
GAC ACG GCC CAC CTG CAG GCA GAG GTC CGC ACG GGC AGC CAC CCG CCC Asp Thr Ala His Leu Gln Ala Glu Val Arg Thr Gly Ser His Pro Pro	625
190 195 200	
CTG CTG CTG TTC GTG GAT CGC TGC GTG GCC ACC CCG ACA CGG GAC CAG Leu Leu Leu Phe Val Asp Arg Cys Val Ala Thr Pro Thr Arg Asp Gln	673
205 210 215	
AGC GGC TCC CCC TAT CAC ACC ATC GTG GAC TTG CAC GGC TGT CTT GTG Ser Gly Ser Pro Tyr His Thr Ile Val Asp Leu His Gly Cys Leu Val	721
220 225 230 235	
GAT GGC CTC TCC GAT GGG GCT TCC AAG TTC AAA GCC CCC AGG CCG AAG Asp Gly Leu Ser Asp Gly Ala Ser Lys Phe Lys Ala Pro Arg Pro Lys	769
240 245 250	
CCG GAC GTG CTC CAG TTC ATG GTG GCC GTG TTC CAC TTC GCT AAT GAC Pro Asp Val Leu Gln Phe Met Val Ala Val Phe His Phe Ala Asn Asp	817
255 260 265	
TCC AGG CAC ACG GTC TAC ATC ACG TGT CAC CTG AGG GTC ATT CCT GCC Ser Arg His Thr Val Tyr Ile Thr Cys His Leu Arg Val Ile Pro Ala	865
270 275 280	

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CAG CAA GCC CCG GAC CGG CTC AAC AAG GCT TGT TCT TTC AAC CAG TCC Gln Gln Ala Pro Asp Arg Leu Asn Lys Ala Cys Ser Phe Asn Gln Ser 285 290 295	913
TCC AGC AGC TGG GCC CCG GTG GAA GGC AGT GCA GAC ATC TGT GAG TGT Ser Ser Ser Trp Ala Pro Val Glu Gly Ser Ala Asp Ile Cys Glu Cys 300 305 310 315	961
TGC GGC AAC GGT GAC TGT GAC CTC ATC GCA GGC TCC CCC ATG AAC CAG Cys Gly Asn Gly Asp Cys Asp Leu Ile Ala Gly Ser Pro Met Asn Gln 320 325 330	1009
AAC CAT GCT GCC CGG TCC TCT CTG CGA AGC CGC AGG CAC GTG ACG GAA Asn His Ala Ala Arg Ser Ser Leu Arg Ser Arg Arg His Val Thr Glu 335 340 345	1057
GAA GCA GAC GTC ACC GTG GGC CCG CTG ATC TTC CTG GGG AAG GCT GGT Glu Ala Asp Val Thr Val Gly Pro Leu Ile Phe Leu Gly Lys Ala Gly 350 355 360	1105
GAC CCT GCC GGC ACA GAG GGG CTG GCC TCT GCT GCG CAG GCG ACC CTG Asp Pro Ala Gly Thr Glu Gly Leu Ala Ser Ala Ala Gln Ala Thr Leu 365 370 375	1153
GTG CTG GGC CTT CGC ATG GCC ACC ATT GTG TTC CTG GCT GTG GCT GCT Val Leu Gly Leu Arg Met Ala Thr Ile Val Phe Leu Ala Val Ala Ala 380 385 390 395	1201
GTG GTC CTG GGC CTC ACC AGG GGG CGC CAC GCT GCT TCC CAC CCC AGG Val Val Leu Gly Leu Thr Arg Gly Arg His Ala Ala Ser His Pro Arg 400 405 410	1249
TCT GCT TCC CAA TAAAAAATCA TGAATTCAAA AAAAAAAAAA AAAAAAAAAA Ser Ala Ser Gln 415	1301
AAAAAAAAAA AAAAAAAAAA AAAGCGGCCG CGAATTC	1338

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Gly Leu Phe Val Cys Leu Leu Leu Trp Gly Gly Ser Glu Leu Cys 1 5 10 15
Cys Pro Gln Pro Leu Trp Phe Trp Gln Gly Gly Thr Arg Gln Pro Ala 20 25 30
Pro Ser Val Thr Pro Val Val Val Glu Cys Leu Glu Ala Arg Leu Val 35 40 45
Val Thr Val Ser Arg Asp Leu Phe Gly Thr Gly Lys Leu Ile Gln Glu 50 55 60
Ala Asp Leu Ser Leu Gly Pro Glu Gly Cys Glu Pro Gln Ala Ser Thr 65 70 75 80
Asp Ala Val Val Arg Phe Glu Val Gly Leu His Glu Cys Gly Asn Ser 85 90 95

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Val Gln Val Thr Asp Asp Ser Leu Val Tyr Ser Ser Phe Leu Leu His
 100 105 110
 Asp Pro Arg Pro Ala Gly Asn Leu Ser Ile Leu Arg Thr Asn Arg Ala
 115 120 125
 Glu Val Pro Ile Glu Cys Arg Tyr Pro Arg Gln Gly Asn Val Ser Ser
 130 135 140
 Arg Ala Ile Leu Pro Thr Trp Val Pro Phe Trp Thr Thr Val Leu Ser
 145 150 155 160
 Glu Glu Arg Leu Val Phe Ser Leu Arg Leu Met Glu Glu Asn Trp Ser
 165 170 175
 Arg Glu Lys Met Ser Pro Thr Phe His Leu Gly Asp Thr Ala His Leu
 180 185 190
 Gln Ala Glu Val Arg Thr Gly Ser His Pro Pro Leu Leu Phe Val
 195 200 205
 Asp Arg Cys Val Ala Thr Pro Thr Arg Asp Gln Ser Gly Ser Pro Tyr
 210 215 220
 His Thr Ile Val Asp Leu His Gly Cys Leu Val Asp Gly Leu Ser Asp
 225 230 235 240
 Gly Ala Ser Lys Phe Lys Ala Pro Arg Pro Lys Pro Asp Val Leu Gln
 245 250 255
 Phe Met Val Ala Val Phe His Phe Ala Asn Asp Ser Arg His Thr Val
 260 265 270
 Tyr Ile Thr Cys His Leu Arg Val Ile Pro Ala Gln Gln Ala Pro Asp
 275 280 285
 Arg Leu Asn Lys Ala Cys Ser Phe Asn Gln Ser Ser Ser Ser Trp Ala
 290 295 300
 Pro Val Glu Gly Ser Ala Asp Ile Cys Glu Cys Cys Gly Asn Gly Asp
 305 310 315 320
 Cys Asp Leu Ile Ala Gly Ser Pro Met Asn Gln Asn His Ala Ala Arg
 325 330 335
 Ser Ser Leu Arg Ser Arg Arg His Val Thr Glu Glu Ala Asp Val Thr
 340 345 350
 Val Gly Pro Leu Ile Phe Leu Gly Lys Ala Gly Asp Pro Ala Gly Thr
 355 360 365
 Glu Gly Leu Ala Ser Ala Ala Gln Ala Thr Leu Val Leu Gly Leu Arg
 370 375 380
 Met Ala Thr Ile Val Phe Leu Ala Val Ala Ala Val Val Leu Gly Leu
 385 390 395 400
 Thr Arg Gly Arg His Ala Ala Ser His Pro Arg Ser Ala Ser Gln
 405 410 415

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Canis familiaris
 - (D) DEVELOPMENTAL STAGE: Juvenile
 - (E) HAPLOTYPE: Diploidy
 - (F) TISSUE TYPE: Ovary
 - (G) CELL TYPE: Oocyte
- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 206..2353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGGG AGCCCTGAAG GAAGCCGCAA GAACCCTGCC CGCACCTCCG CGACCTCAAG	60
ATGTCCACTC CACTGGAAGA CGGAGAATAC TGGATTGACC CCAACCAAGG ATGCAACCTG	120
ATGCCATCAA GGTTTTCTGC AACATGGAGA CAGGTGAGAC CTGCGTATAC CCACCTACCT	180
GGCTGATTG GTGGTACGTT TGGCC ATG GCA TGC AAA CAG AAA GGA GAC AGT	232
Met Ala Cys Lys Gln Lys Gly Asp Ser	
1 5	
GGG AGT CCC TCA AGC AGG TTT AGT GCA GAT TGG AGC ACC TAC AGG TCA	280
Gly Ser Pro Ser Ser Arg Phe Ser Ala Asp Trp Ser Thr Tyr Arg Ser	
10 15 20 25	
CTT TCT TTA TTC TTC ATC CTT GTG ACT TCA GTG AAC TCA GTA GGT GTT	328
Leu Ser Leu Phe Phe Ile Leu Val Thr Ser Val Asn Ser Val Gly Val	
30 35 40	
ATG CAG TTG GTG AAT CCC ATC TTC CCA GGT ACT GTC ATT TGC CAT GAA	376
Met Gln Leu Val Asn Pro Ile Phe Pro Gly Thr Val Ile Cys His Glu	
45 50 55	
AAT AAA ATG ACA GTG GAA TTT CCA AGG GAT CTT GGC ACC AAA AAA TGG	424
Asn Lys Met Thr Val Glu Phe Pro Arg Asp Leu Gly Thr Lys Lys Trp	
60 65 70	
CAT GCA TCT GTG GTG GAT CCA TTT AGT TTT GAA TTG TTG AAC TGT ACT	472
His Ala Ser Val Val Asp Pro Phe Ser Phe Glu Leu Leu Asn Cys Thr	
75 80 85	
TCT ATC CTG GAC CCA GAA AAG CTC ACC CTG AAG GCC CCA TAT GAG ACC	520
Ser Ile Leu Asp Pro Glu Lys Leu Thr Leu Lys Ala Pro Tyr Glu Thr	
90 95 100 105	
TGT AGC AGG AGA GTG CTT GGC CAG CAT CAG ATG GCC ATC AGA CTC ACG	568
Cys Ser Arg Arg Val Leu Gly Gln His Gln Met Ala Ile Arg Leu Thr	
110 115 120	
GAC AAC AAT GCT GCT TCA AGA CAT AAG GCT TTC ATG TAT CAG ATC AGC	616
Asp Asn Asn Ala Ala Ser Arg His Lys Ala Phe Met Tyr Gln Ile Ser	
125 130 135	
TGT CCA GTT ATG CAA ACA GAA GAA ACC CAT GAG CAT GCA GGA TCC ACA	664
Cys Pro Val Met Gln Thr Glu Glu Thr His Glu His Ala Gly Ser Thr	
140 145 150	
ATC TGC ACA AAA GAT TCC ATG TCT TTT ACC TTT AAC ATT ATT CCT GGC	712

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Ile Cys Thr Lys Asp Ser Met Ser Phe Thr Phe Asn Ile Ile Pro Gly 155 160 165	
ATG GCT GAT GAA AAT ACG AAT CCC AGT GGT GGG AAA TGG ATG ATG GAG Met Ala Asp Glu Asn Thr Asn Pro Ser Gly Gly Lys Trp Met Met Glu 170 175 180 185	760
GTT GAT GAT GCA AAA GCT CAA AAT CTG ACT CTT CGG GAG GCC TTG ATG Val Asp Asp Ala Lys Ala Gln Asn Leu Thr Leu Arg Glu Ala Leu Met 190 195 200	808
CAA GGA TAT AAT TTC CTG TTT GAT AGC CAC AGG CTC AGT GTC CAA GTG Gln Gly Tyr Asn Phe Leu Phe Asp Ser His Arg Leu Ser Val Gln Val 205 210 215	856
TCA TTC AAT GCC ACT GGA GTC ACT CAC TAC ATG CAA GGT AAC AGT CAC Ser Phe Asn Ala Thr Gly Val Thr His Tyr Met Gln Gly Asn Ser His 220 225 230	904
CTC TAC ACA GTG CCT CTG AAG CTT ATA CAC ACA TCT CCT GGG CAG AAG Leu Tyr Thr Val Pro Leu Lys Leu Ile His Thr Ser Pro Gly Gln Lys 235 240 245	952
ATC ATC TTA ACA ACA CGA GTA CTT TGT ATG TCA GAT CCC GTG ACC TGT Ile Ile Leu Thr Thr Arg Val Leu Cys Met Ser Asp Pro Val Thr Cys 250 255 260 265	1000
AAC GCC ACA CAC ATG ACC CTC ACC ATA CCA GAG TTT CCT GGG AAA CTA Asn Ala Thr His Met Thr Leu Thr Ile Pro Glu Phe Pro Gly Lys Leu 270 275 280	1048
CAG TCT GTG AGA TTT GAA AAC ACG AAC TTT CGT GTA AGC CAG CTG CAC Gln Ser Val Arg Phe Glu Asn Thr Asn Phe Arg Val Ser Gln Leu His 285 290 295	1096
AAC CAT GGG ATT GAT AAA GAA GAA TTA AAC GGC TTG AGG TTA CAC TTC Asn His Gly Ile Asp Lys Glu Glu Leu Asn Gly Leu Arg Leu His Phe 300 305 310	1144
AGC AAA TCT CTT CTC AAA ATG AAC TCC TCT GAA AAA TGC CTA CTC TAT Ser Lys Ser Leu Leu Lys Met Asn Ser Ser Glu Lys Cys Leu Leu Tyr 315 320 325	1192
CAG TTC TAC TTA GCA TCT CTC AAG CTG ACC TTT GCC TTT GAA CGG GAC Gln Phe Tyr Leu Ala Ser Leu Lys Leu Thr Phe Ala Phe Glu Arg Asp 330 335 340 345	1240
ACG GTT TCC ACA GTG GTT TAT CCT GAG TGT GTT TGT GAG CCA CCA GTT Thr Val Ser Thr Val Val Tyr Pro Glu Cys Val Cys Glu Pro Pro Val 350 355 360	1288
ACT ATA GTT ACA GGT GAC CTG TGT ACC CAG GAT GGG TTT ATG GAT GTC Thr Ile Val Thr Gly Asp Leu Cys Thr Gln Asp Gly Phe Met Asp Val 365 370 375	1336
AAG GTC TAC AGC CAC CAA ACA AAA CCA GCT CTA AAC TTG GAT ACC CTC Lys Val Tyr Ser His Gln Thr Lys Pro Ala Leu Asn Leu Asp Thr Leu 380 385 390	1384
AGA GTG GGA GAC TCC TCC TGC CAA CCT ACT TTC AAG GCT CCA TCA CAA Arg Val Gly Asp Ser Ser Cys Gln Pro Thr Phe Lys Ala Pro Ser Gln 395 400 405	1432
GGG TTG ACA CTG TTT CAC ATC CCC CTA AAT GGA TGT GGA ACA AGA CTT Gly Leu Thr Leu Phe His Ile Pro Leu Asn Gly Cys Gly Thr Arg Leu 410 415 420 425	1480

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AAG TTC AAA GGT GAC ACA GTC ATC TAT GAA AAT GAA ATA CAT GCT CTC Lys Phe Lys Gly Asp Thr Val Ile Tyr Glu Asn Glu Ile His Ala Leu 430 435 440	1528
TGG ACA GAT CTC CCT CCA AGC ACA ATT TCC AGA GAT AGT GAA TTC AGA Trp Thr Asp Leu Pro Pro Ser Thr Ile Ser Arg Asp Ser Glu Phe Arg 445 450 455	1576
ATG ACT GTG AAG TGC CAT TAC AGC AGA GAT GAC CTG CTG ATA AAT ACC Met Thr Val Lys Cys His Tyr Ser Arg Asp Asp Leu Leu Ile Asn Thr 460 465 470	1624
AAT GTC CAA AGT CTT CCT CCT CCC GTG GCC TCA GTG AGG CCT GGT CCA Asn Val Gln Ser Leu Pro Pro Pro Val Ala Ser Val Arg Pro Gly Pro 475 480 485	1672
CTT GCC TTA ATC CTG CAA ACC TAC CCA GAT AAA TCC TAT TTG CGA CCC Leu Ala Leu Ile Leu Gln Thr Tyr Pro Asp Lys Ser Tyr Leu Arg Pro 490 495 500 505	1720
TAT GGG GAT AAG GAG TAT CCT GTG GTG AGA TAC CTC CGC CAA CCA ATT Tyr Gly Asp Lys Glu Tyr Pro Val Val Arg Tyr Leu Arg Gln Pro Ile 510 515 520	1768
TAC CTG GAA GTG AAA GTC CTA AAT AGG GCT GAC CCC AAC ATC AAG CTG Tyr Leu Glu Val Lys Val Leu Asn Arg Ala Asp Pro Asn Ile Lys Leu 525 530 535	1816
GTC TTA GAT GAT TGC TGG GCA ACA CCC ACC ATG GAC CCA GCC TCA CTC Val Leu Asp Asp Cys Trp Ala Thr Pro Thr Met Asp Pro Ala Ser Leu 540 545 550	1864
CCC CAG TGG AAT ATT GTC ATG GAT GGC TGT GAA TAC AAT CTG GAC AAC Pro Gln Trp Asn Ile Val Met Asp Gly Cys Glu Tyr Asn Leu Asp Asn 555 560 565	1912
TAC AGA ACG ACC TTC CAT CCA GTT GGC TCC TCT GTG ACC TAC CCT ACT Tyr Arg Thr Thr Phe His Pro Val Gly Ser Ser Val Thr Tyr Pro Thr 570 575 580 585	1960
CAC TAT CAG AGG TTT GAT GTG AAG ACC TTT GCC TTT ATA TCA GAG GCC His Tyr Gln Arg Phe Asp Val Lys Thr Phe Ala Phe Ile Ser Glu Ala 590 595 600	2008
CAA GTG CTT TCT AGC CTG GTC TAC TTC CAC TGC ACC GCA TTA ATC TGC Gln Val Leu Ser Ser Leu Val Tyr Phe His Cys Thr Ala Leu Ile Cys 605 610 615	2056
AAT CGA CTG TCT CCT GAC TCC CCT CTG TGT TCT GTG ACT TGC CCT GTA Asn Arg Leu Ser Pro Asp Ser Pro Leu Cys Ser Val Thr Cys Pro Val 620 625 630	2104
TCA TCC AGG CAC AGG CGA GCC ACA GGC AGT ACT GAA GAA GAG AAG ATG Ser Ser Arg His Arg Arg Ala Thr Gly Ser Thr Glu Glu Glu Lys Met 635 640 645	2152
ATA GTA AGT CTC CCG GGA CCC ATC CTC CTG TTG GCA GAC AGC TCT TCA Ile Val Ser Leu Pro Gly Pro Ile Leu Leu Leu Ala Asp Ser Ser Ser 650 655 660 665	2200
CTC AGA GAT GGT GTG GAC TCA AAA GGG CAC AGG GCT GCT GGA TAT GTT Leu Arg Asp Gly Val Asp Ser Lys Gly His Arg Ala Ala Gly Tyr Val 670 675 680	2248
GCT TTT AAA ACT GTA GTG GCT GTG GCT GCC TTA GCA GGC CTT GTG GCT Ala Phe Lys Thr Val Val Ala Val Ala Ala Leu Ala Gly Leu Val Ala 685 690 695	2296

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GCT CTA GGT CTC ATC ATC TAC CTG CGT AAG AAA AGA ACC ATG GTG TTA 2344
 Ala Leu Gly Leu Ile Ile Tyr Leu Arg Lys Lys Arg Thr Met Val Leu
 700 705 710

AAT CAC TAAGGATTTT CAAATAAAGT GTCCGGAATT C 2381
 Asn His
 715

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 715 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Cys Lys Gln Lys Gly Asp Ser Gly Ser Pro Ser Ser Arg Phe
 1 5 10 15
 Ser Ala Asp Trp Ser Thr Tyr Arg Ser Leu Ser Leu Phe Phe Ile Leu
 20 25 30
 Val Thr Ser Val Asn Ser Val Gly Val Met Gln Leu Val Asn Pro Ile
 35 40 45
 Phe Pro Gly Thr Val Ile Cys His Glu Asn Lys Met Thr Val Glu Phe
 50 55 60
 Pro Arg Asp Leu Gly Thr Lys Lys Trp His Ala Ser Val Val Asp Pro
 65 70 75 80
 Phe Ser Phe Glu Leu Leu Asn Cys Thr Ser Ile Leu Asp Pro Glu Lys
 85 90 95
 Leu Thr Leu Lys Ala Pro Tyr Glu Thr Cys Ser Arg Arg Val Leu Gly
 100 105 110
 Gln His Gln Met Ala Ile Arg Leu Thr Asp Asn Asn Ala Ala Ser Arg
 115 120 125
 His Lys Ala Phe Met Tyr Gln Ile Ser Cys Pro Val Met Gln Thr Glu
 130 135 140
 Glu Thr His Glu His Ala Gly Ser Thr Ile Cys Thr Lys Asp Ser Met
 145 150 155 160
 Ser Phe Thr Phe Asn Ile Ile Pro Gly Met Ala Asp Glu Asn Thr Asn
 165 170 175
 Pro Ser Gly Gly Lys Trp Met Met Glu Val Asp Asp Ala Lys Ala Gln
 180 185 190
 Asn Leu Thr Leu Arg Glu Ala Leu Met Gln Gly Tyr Asn Phe Leu Phe
 195 200 205
 Asp Ser His Arg Leu Ser Val Gln Val Ser Phe Asn Ala Thr Gly Val
 210 215 220
 Thr His Tyr Met Gln Gly Asn Ser His Leu Tyr Thr Val Pro Leu Lys
 225 230 235 240
 Leu Ile His Thr Ser Pro Gly Gln Lys Ile Ile Leu Thr Thr Arg Val
 245 250 255

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Leu Cys Met Ser Asp Pro Val Thr Cys Asn Ala Thr His Met Thr Leu
 260 265 270
 Thr Ile Pro Glu Phe Pro Gly Lys Leu Gln Ser Val Arg Phe Glu Asn
 275 280 285
 Thr Asn Phe Arg Val Ser Gln Leu His Asn His Gly Ile Asp Lys Glu
 290 295 300
 Glu Leu Asn Gly Leu Arg Leu His Phe Ser Lys Ser Leu Leu Lys Met
 305 310 315 320
 Asn Ser Ser Glu Lys Cys Leu Leu Tyr Gln Phe Tyr Leu Ala Ser Leu
 325 330 335
 Lys Leu Thr Phe Ala Phe Glu Arg Asp Thr Val Ser Thr Val Val Tyr
 340 345 350
 Pro Glu Cys Val Cys Glu Pro Pro Val Thr Ile Val Thr Gly Asp Leu
 355 360 365
 Cys Thr Gln Asp Gly Phe Met Asp Val Lys Val Tyr Ser His Gln Thr
 370 375 380
 Lys Pro Ala Leu Asn Leu Asp Thr Leu Arg Val Gly Asp Ser Ser Cys
 385 390 395 400
 Gln Pro Thr Phe Lys Ala Pro Ser Gln Gly Leu Thr Leu Phe His Ile
 405 410 415
 Pro Leu Asn Gly Cys Gly Thr Arg Leu Lys Phe Lys Gly Asp Thr Val
 420 425 430
 Ile Tyr Glu Asn Glu Ile His Ala Leu Trp Thr Asp Leu Pro Pro Ser
 435 440 445
 Thr Ile Ser Arg Asp Ser Glu Phe Arg Met Thr Val Lys Cys His Tyr
 450 455 460
 Ser Arg Asp Asp Leu Leu Ile Asn Thr Asn Val Gln Ser Leu Pro Pro
 465 470 475 480
 Pro Val Ala Ser Val Arg Pro Gly Pro Leu Ala Leu Ile Leu Gln Thr
 485 490 495
 Tyr Pro Asp Lys Ser Tyr Leu Arg Pro Tyr Gly Asp Lys Glu Tyr Pro
 500 505 510
 Val Val Arg Tyr Leu Arg Gln Pro Ile Tyr Leu Glu Val Lys Val Leu
 515 520 525
 Asn Arg Ala Asp Pro Asn Ile Lys Leu Val Leu Asp Asp Cys Trp Ala
 530 535 540
 Thr Pro Thr Met Asp Pro Ala Ser Leu Pro Gln Trp Asn Ile Val Met
 545 550 555 560
 Asp Gly Cys Glu Tyr Asn Leu Asp Asn Tyr Arg Thr Thr Phe His Pro
 565 570 575
 Val Gly Ser Ser Val Thr Tyr Pro Thr His Tyr Gln Arg Phe Asp Val
 580 585 590
 Lys Thr Phe Ala Phe Ile Ser Glu Ala Gln Val Leu Ser Ser Leu Val
 595 600 605

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Tyr Phe His Cys Thr Ala Leu Ile Cys Asn Arg Leu Ser Pro Asp Ser
 610 615 620
 Pro Leu Cys Ser Val Thr Cys Pro Val Ser Ser Arg His Arg Arg Ala
 625 630 635 640
 Thr Gly Ser Thr Glu Glu Glu Lys Met Ile Val Ser Leu Pro Gly Pro
 645 650 655
 Ile Leu Leu Leu Ala Asp Ser Ser Ser Leu Arg Asp Gly Val Asp Ser
 660 665 670
 Lys Gly His Arg Ala Ala Gly Tyr Val Ala Phe Lys Thr Val Val Ala
 675 680 685
 Val Ala Ala Leu Ala Gly Leu Val Ala Ala Leu Gly Leu Ile Ile Tyr
 690 695 700
 Leu Arg Lys Lys Arg Thr Met Val Leu Asn His
 705 710 715

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Canis familiaris
- (D) DEVELOPMENTAL STAGE: Juvenile
- (E) HAPLOTYPE: Diploidy
- (F) TISSUE TYPE: Ovary
- (G) CELL TYPE: Oocyte

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 13..1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCGGG CT ATG GGG CTG AGC TAT GGA ATT TTC ATC TGT TTT CTG	48
Met Gly Leu Ser Tyr Gly Ile Phe Ile Cys Phe Leu	
1 5 10	
CTC CTG GGA GGC ATG GAG CTG TGC TGC CCC CAG ACC ATC TGG CCA ACT	96
Leu Leu Gly Gly Met Glu Leu Cys Cys Pro Gln Thr Ile Trp Pro Thr	
15 20 25	
GAG ACC TAC TAC CCA TTG ACA TCT AGG CCC CCA GTA ATG GTG GAC TGT	144
Glu Thr Tyr Tyr Pro Leu Thr Ser Arg Pro Pro Val Met Val Asp Cys	
30 35 40	
CTG GAG TCC CAG CTG GTG GTC ACT GTC AGC AAA GAC CTT TTT GGT ACT	192
Leu Glu Ser Gln Leu Val Val Thr Val Ser Lys Asp Leu Phe Gly Thr	
45 50 55 60	
GGG AAG CTC ATC AGG CCA GCA GAC CTC ACC CTG GGT CCA GAG AAC TGT	240

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Gly Lys Leu Ile Arg Pro Ala Asp Leu Thr Leu Gly Pro Glu Asn Cys	
65 70 75	
GAG CCC CTG GTC TCC ATG GAC ACG GAT GAT GTG GTC AGG TTT GAG GTT	288
Glu Pro Leu Val Ser Met Asp Thr Asp Asp Val Val Arg Phe Glu Val	
80 85 90	
GGG CTG CAC GAG TGT GGC AGC AGG GTG CAG GTG ACT GAC AAT GCT CTG	336
Gly Leu His Glu Cys Gly Ser Arg Val Gln Val Thr Asp Asn Ala Leu	
95 100 105	
GTG TAC AGC ACC TTC CTG ATC CAC AGC CCC CGC CCT GCG GGC AAC CTG	384
Val Tyr Ser Thr Phe Leu Ile His Ser Pro Arg Pro Ala Gly Asn Leu	
110 115 120	
TCC ATC CTG AGA ACT AAT CGT GCC GAG GTT CCC ATC GAG TGC CAC TAC	432
Ser Ile Leu Arg Thr Asn Arg Ala Glu Val Pro Ile Glu Cys His Tyr	
125 130 135 140	
CCC AGG CAC AGC AAT GTG AGC AGC CAG GCC ATC CTG CCC ACT TGG GTG	480
Pro Arg His Ser Asn Val Ser Ser Gln Ala Ile Leu Pro Thr Trp Val	
145 150 155	
CCC TTC AGG ACC ACA ATG CTC TTC GAG GAG AAG CTA GTT TTC TCT CTC	528
Pro Phe Arg Thr Thr Met Leu Phe Glu Glu Lys Leu Val Phe Ser Leu	
160 165 170	
CGC CTA ATG GAG GAG GAC TGG GGC TCC GAG AAG CAA TCC CCC ACA TTC	576
Arg Leu Met Glu Glu Asp Trp Gly Ser Glu Lys Gln Ser Pro Thr Phe	
175 180 185	
CAG CTG GGA GAC ATA GCC CAC CTC CAG GCT GAA GTC CAC ACT GGC AGC	624
Gln Leu Gly Asp Ile Ala His Leu Gln Ala Glu Val His Thr Gly Ser	
190 195 200	
CAT ATG CCA CTG CGA CTT TTT GTG GAC CAC TGT GTG GCC ACG CTG ACA	672
His Met Pro Leu Arg Leu Phe Val Asp His Cys Val Ala Thr Leu Thr	
205 210 215 220	
CCA GAT CGG AAT GCC TTC CTT CAT CAC AAA ATT GTG GAC TTC CAT GGC	720
Pro Asp Arg Asn Ala Phe Leu His His Lys Ile Val Asp Phe His Gly	
225 230 235	
TGT CTT GTG GAT GGT CTC TAC AAT TCC TCT TCA GCC TTC AAA GCC CCC	768
Cys Leu Val Asp Gly Leu Tyr Asn Ser Ser Ser Ala Phe Lys Ala Pro	
240 245 250	
AGA CCC AGG CCA GAG ACT CTT CAG TTC ACA GTG GAT GTT TTC CAC TTT	816
Arg Pro Arg Pro Glu Thr Leu Gln Phe Thr Val Asp Val Phe His Phe	
255 260 265	
GCT AAG GAC TCA AGA AAC ACG ATC TAT ATC ACC TGC CAT CTG AAG GTC	864
Ala Lys Asp Ser Arg Asn Thr Ile Tyr Ile Thr Cys His Leu Lys Val	
270 275 280	
ACT CCG GCT GAC CGA GTC CCA GAC CAG CTA AAC AAA GCT TGT TCC TTC	912
Thr Pro Ala Asp Arg Val Pro Asp Gln Leu Asn Lys Ala Cys Ser Phe	
285 290 295 300	
ATC AAG TCT ACC AAG AGG TGG TAC CCT GTA GAA GGC TCG GCT GAT ATT	960
Ile Lys Ser Thr Lys Arg Trp Tyr Pro Val Glu Gly Ser Ala Asp Ile	
305 310 315	
TGT CGC TGT TGT AAC AAA GGC AGC TGT GGC CTT CCA GGC CGG TCC AGG	1008
Cys Arg Cys Cys Asn Lys Gly Ser Cys Gly Leu Pro Gly Arg Ser Arg	
320 325 330	

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AGG CTG TCC CAC CTA GAG AGA GGG TGG CGC AAG TCT GTT TCC CAC ACT	1056
Arg Leu Ser His Leu Glu Arg Gly Trp Arg Lys Ser Val Ser His Thr	
335 340 345	
AGA AAT CGC AGG CAC GTG ACT GAA GAA GCA GAG ATC ACC GTG GGG CCT	1104
Arg Asn Arg Arg His Val Thr Glu Glu Ala Glu Ile Thr Val Gly Pro	
350 355 360	
CTG ATC TTC CTG GGA AAG GCT AGT GAT CAT GGT ATA GAG GGG TCA ACC	1152
Leu Ile Phe Leu Gly Lys Ala Ser Asp His Gly Ile Glu Gly Ser Thr	
365 370 375 380	
TCT CCT CAC ACC TCT GTG ATG TTG GGC TTA GGC CTG GCC ACG GTG GTA	1200
Ser Pro His Thr Ser Val Met Leu Gly Leu Ala Thr Val Val	
385 390 395	
TCC CTG ACT CTA GCT ACC ATT GTC CTG GTC CTT GCC AAG AGG CAT CGT	1248
Ser Leu Thr Leu Ala Thr Ile Val Leu Val Leu Ala Lys Arg His Arg	
400 405 410	
ACT GCT TCC CAC CCT GTG ATA TGC CCT GCA TCT GTC TCC CAA TAAAAGAATA	1300
Thr Ala Ser His Pro Val Ile Cys Pro Ala Ser Val Ser Gln	
415 420 425	
AGCAAAAAAA AAAAAACCGG AATTC	1325

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Leu Ser Tyr Gly Ile Phe Ile Cys Phe Leu Leu Leu Gly Gly	
1 5 10 15	
Met Glu Leu Cys Cys Pro Gln Thr Ile Trp Pro Thr Glu Thr Tyr Tyr	
20 25 30	
Pro Leu Thr Ser Arg Pro Pro Val Met Val Asp Cys Leu Glu Ser Gln	
35 40 45	
Leu Val Val Thr Val Ser Lys Asp Leu Phe Gly Thr Gly Lys Leu Ile	
50 55 60	
Arg Pro Ala Asp Leu Thr Leu Gly Pro Glu Asn Cys Glu Pro Leu Val	
65 70 75 80	
Ser Met Asp Thr Asp Asp Val Val Arg Phe Glu Val Gly Leu His Glu	
85 90 95	
Cys Gly Ser Arg Val Gln Val Thr Asp Asn Ala Leu Val Tyr Ser Thr	
100 105 110	
Phe Leu Ile His Ser Pro Arg Pro Ala Gly Asn Leu Ser Ile Leu Arg	
115 120 125	
Thr Asn Arg Ala Glu Val Pro Ile Glu Cys His Tyr Pro Arg His Ser	
130 135 140	
Asn Val Ser Ser Gln Ala Ile Leu Pro Thr Trp Val Pro Phe Arg Thr	
145 150 155 160	

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Thr Met Leu Phe Glu Glu Lys Leu Val Phe Ser Leu Arg Leu Met Glu
 165 170 175
 Glu Asp Trp Gly Ser Glu Lys Gln Ser Pro Thr Phe Gln Leu Gly Asp
 180 185 190
 Ile Ala His Leu Gln Ala Glu Val His Thr Gly Ser His Met Pro Leu
 195 200 205
 Arg Leu Phe Val Asp His Cys Val Ala Thr Leu Thr Pro Asp Arg Asn
 210 215 220
 Ala Phe Leu His His Lys Ile Val Asp Phe His Gly Cys Leu Val Asp
 225 230 235 240
 Gly Leu Tyr Asn Ser Ser Ser Ala Phe Lys Ala Pro Arg Pro Arg Pro
 245 250 255
 Glu Thr Leu Gln Phe Thr Val Asp Val Phe His Phe Ala Lys Asp Ser
 260 265 270
 Arg Asn Thr Ile Tyr Ile Thr Cys His Leu Lys Val Thr Pro Ala Asp
 275 280 285
 Arg Val Pro Asp Gln Leu Asn Lys Ala Cys Ser Phe Ile Lys Ser Thr
 290 295 300
 Lys Arg Trp Tyr Pro Val Glu Gly Ser Ala Asp Ile Cys Arg Cys Cys
 305 310 315 320
 Asn Lys Gly Ser Cys Gly Leu Pro Gly Arg Ser Arg Arg Leu Ser His
 325 330 335
 Leu Glu Arg Gly Trp Arg Lys Ser Val Ser His Thr Arg Asn Arg Arg
 340 345 350
 His Val Thr Glu Glu Ala Glu Ile Thr Val Gly Pro Leu Ile Phe Leu
 355 360 365
 Gly Lys Ala Ser Asp His Gly Ile Glu Gly Ser Thr Ser Pro His Thr
 370 375 380
 Ser Val Met Leu Gly Leu Gly Leu Ala Thr Val Val Ser Leu Thr Leu
 385 390 395 400
 Ala Thr Ile Val Leu Val Leu Ala Lys Arg His Arg Thr Ala Ser His
 405 410 415
 Pro Val Ile Cys Pro Ala Ser Val Ser Gln
 420 425

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Felis domesticus
 (D) DEVELOPMENTAL STAGE: Juvenile
 (E) HAPLOTYPE: Diploidy
 (F) TISSUE TYPE: Ovary
 (G) CELL TYPE: Oocyte

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 28..2175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCGCGG CCGCGATACT TTTGGCT ATG GCC TCC AGA CAG AAA GGA GAT	51
Met Ala Ser Arg Gln Lys Gly Asp	
1 5	
AGT GGG AGT CCT TCA AGC TGG TTT AAT GCA GAT TGG AGC ACC TAC AGG	99
Ser Gly Ser Pro Ser Ser Trp Phe Asn Ala Asp Trp Ser Thr Tyr Arg	
10 15 20	
TCA CTT TTT CTA CTC TTT ATC CTC GTG ACT TCA GTG AAT TCC ATA GGT	147
Ser Leu Phe Leu Leu Phe Ile Leu Val Thr Ser Val Asn Ser Ile Gly	
25 30 35 40	
GTT TTG CAG TTG GTG AAT CCT GTC TTC CCA GGT ACT GTC ACT TGC TAT	195
Val Leu Gln Leu Val Asn Pro Val Phe Pro Gly Thr Val Thr Cys Tyr	
45 50 55	
GAA ACT AGA ATG GCA GTG GAA TTT CCA AGT GAT TTT GGC ACC AAA AAA	243
Glu Thr Arg Met Ala Val Glu Phe Pro Ser Asp Phe Gly Thr Lys Lys	
60 65 70	
TGG CAT ACA TCT GTG GTG GAT CCC TTT AGT TTT GAA TTG TTG AAC TGC	291
Trp His Thr Ser Val Val Asp Pro Phe Ser Phe Glu Leu Leu Asn Cys	
75 80 85	
ACT TAC ATC TTG GAT CCA GAA AAT CTC ACC TTA AAG GCC CCA TAT GAG	339
Thr Tyr Ile Leu Asp Pro Glu Asn Leu Thr Leu Lys Ala Pro Tyr Glu	
90 95 100	
ACC TGT ACC AGA AGA ACG CTT GGC CAG CAC CGG ATG ATC ATC AGA CTC	387
Thr Cys Thr Arg Arg Thr Leu Gly Gln His Arg Met Ile Ile Arg Leu	
105 110 115 120	
AAG GAC CAC AAT GCT GCT TCA AGA CAT AAC AGT TTG ATG TAT CAG ATC	435
Lys Asp His Asn Ala Ala Ser Arg His Asn Ser Leu Met Tyr Gln Ile	
125 130 135	
AAC TGT CCA GTT ATG CAA GCA GAA GAA ACC CAT GAG CAT GCA GGA TCC	483
Asn Cys Pro Val Met Gln Ala Glu Glu Thr His Glu His Ala Gly Ser	
140 145 150	
ACT ATC TGC ACA AAG GAT TCC ATG TCT TTT ACC TTT AAT GTC ATT CCT	531
Thr Ile Cys Thr Lys Asp Ser Met Ser Phe Thr Phe Asn Val Ile Pro	
155 160 165	
GGC CTG GCT GAT GAA AAT ACG GAT ATC AAG AAT CCG ATG GGA TGG AGC	579
Gly Leu Ala Asp Glu Asn Thr Asp Ile Lys Asn Pro Met Gly Trp Ser	
170 175 180	
ATT GAG GTT GGT GAT GGT ACA AAA GCC AAA ACT CTG ACT CTT CAG GAT	627
Ile Glu Val Gly Asp Gly Thr Lys Ala Lys Thr Leu Thr Leu Gln Asp	
185 190 195 200	
GTC TTG AGA CAA GGA TAC AAT ATC CTG TTT GAT AAC CAC AAG ATC ACC	675
Val Leu Arg Gln Gly Tyr Asn Ile Leu Phe Asp Asn His Lys Ile Thr	

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205	210	215	
TTC CAG GTG TCA TTC AAT GCC ACT GGA GTG ACT CAC TAC ATG CAA GGT Phe Gln Val Ser Phe Asn Ala Thr Gly Val Thr His Tyr Met Gln Gly 220 225 230			723
AAC AGT CAC CTC TAC ATG GTG CCT CTG AAG TTG ATA CAT GAA TCT CTT Asn Ser His Leu Tyr Met Val Pro Leu Lys Leu Ile His Glu Ser Leu 235 240 245			771
GGG CAG AAG ATC ATC TTA ACA ACA CGA GTG CTT TGT ATG TCA GAT GCT Gly Gln Lys Ile Ile Leu Thr Thr Arg Val Leu Cys Met Ser Asp Ala 250 255 260			819
GTG ACC TGT AAT GCC ACA CAT GTG ACT CTG ACC ATA CCA GAG TTT CCT Val Thr Cys Asn Ala Thr His Val Thr Leu Thr Ile Pro Glu Phe Pro 265 270 275 280			867
GGG AAG TTA AAA TCT GTG AGC TCT GAA AAT AGG AAC TTT GCT GTA AGC Gly Lys Leu Lys Ser Val Ser Ser Glu Asn Arg Asn Phe Ala Val Ser 285 290 295			915
CAG CTG CAC AAC AAT GGG ATT GAT AAA GAA GAA TCA AGT GGC TTG ACA Gln Leu His Asn Asn Gly Ile Asp Lys Glu Glu Ser Ser Gly Leu Thr 300 305 310			963
TTG CAC TTC AGC AAA ACT CTT CTC AAA ATG GAA TTC TCT GAA AAA TGC Leu His Phe Ser Lys Thr Leu Leu Lys Met Glu Phe Ser Glu Lys Cys 315 320 325			1011
CTA CCC TAT CAG TTC TAC TTA GCT TCA CTC AAG CTG ACC TTT GCC TTT Leu Pro Tyr Gln Phe Tyr Leu Ala Ser Leu Lys Leu Thr Phe Ala Phe 330 335 340			1059
AAT CAA GAG ACT ATA TCC ACG GTG CTT TAT CCT GAG TGT GTC TGT GAG Asn Gln Glu Thr Ile Ser Thr Val Leu Tyr Pro Glu Cys Val Cys Glu 345 350 355 360			1107
TCA CCA GTT TCT ATA GTT ACA GGT GAC CTG TGT ACT CAG GAT GGG TTT Ser Pro Val Ser Ile Val Thr Gly Asp Leu Cys Thr Gln Asp Gly Phe 365 370 375			1155
ATG GAC ATA AAG GTC TAC AGT CAC CAG ACA AAA CCA GCT CTC AAC TTA Met Asp Ile Lys Val Tyr Ser His Gln Thr Lys Pro Ala Leu Asn Leu 380 385 390			1203
GAA ACC CTA AGG GTG GGA GAC TCA TCC TGC CAA CCT ACC TTC CAG GCT Glu Thr Leu Arg Val Gly Asp Ser Ser Cys Gln Pro Thr Phe Gln Ala 395 400 405			1251
GCA TCT CAA GGG CTG ATA CTG TTT CAC ATA CCC CTG AAT GGA TGC GGG Ala Ser Gln Gly Leu Ile Leu Phe His Ile Pro Leu Asn Gly Cys Gly 410 415 420			1299
ACA AGA CAT AAG TTC AAG GAA GGC AAA GTC ATC TAT GAA AAT GAA ATA Thr Arg His Lys Phe Lys Glu Gly Lys Val Ile Tyr Glu Asn Glu Ile 425 430 435 440			1347
CAT GCT GTC TGG GCG GAT CTT CCT CCA AGC ACA ATT TCT AGA GAT AGT His Ala Val Trp Ala Asp Leu Pro Pro Ser Thr Ile Ser Arg Asp Ser 445 450 455			1395
GAA TTC AGA ATG ACA GTG CAG TGC CAT TAC AGC AAA GGT GAC CTG CTA Glu Phe Arg Met Thr Val Gln Cys His Tyr Ser Lys Gly Asp Leu Leu 460 465 470			1443
ATA AAT ACC AGA GTC CAA AGT CTT CCT CCT CTA GAG GCC TCA GTG AGG			1491

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Ile Asn Thr Arg Val Gln Ser Leu Pro Pro Leu Glu Ala Ser Val Arg 475 480 485	
CCA GGT CCA CTT GCC TTA ATC CTG CAA ACC TAC CCA GAT AAA TCC TAC Pro Gly Pro Leu Ala Leu Ile Leu Gln Thr Tyr Pro Asp Lys Ser Tyr 490 495 500	1539
CTC CAA CCT TAC GGG GAG AAG GAG TAC CCT GTG GTG AGA TAC CTC CGC Leu Gln Pro Tyr Gly Glu Lys Glu Tyr Pro Val Val Arg Tyr Leu Arg 505 510 515 520	1587
CAA CCA ATT TAT CTG GAA GTG AGA GTC CTA AAT AGG TCT GAC CCC AAC Gln Pro Ile Tyr Leu Glu Val Arg Val Leu Asn Arg Ser Asp Pro Asn 525 530 535	1635
ATC AAG CTG GTC TTA GAT GAC TGC TGG GCA ACA CCC ACG ATG GAC CCA Ile Lys Leu Val Leu Asp Asp Cys Trp Ala Thr Pro Thr Met Asp Pro 540 545 550	1683
GCC TCC GTC CCC CAG TGG AAT ATT ATC ATG GAT GGC TGT GAA TAC AAC Ala Ser Val Pro Gln Trp Asn Ile Ile Met Asp Gly Cys Glu Tyr Asn 555 560 565	1731
CTG GAC AAC CAC AGA ACC ACC TTC CAT CCA GTT GGC TCC TCT GTG ACC Leu Asp Asn His Arg Thr Thr Phe His Pro Val Gly Ser Ser Val Thr 570 575 580	1779
TAT CCT ACT CAC TAT CGG AGG TTT GAT GTG AAG ACC TTT GCC TTT GTA Tyr Pro Thr His Tyr Arg Arg Phe Asp Val Lys Thr Phe Ala Phe Val 585 590 595 600	1827
TCA GAG GCC CAA GTG CTT TCT AGT CTG GTC TAC TTC CAC TGC AGT GTC Ser Glu Ala Gln Val Leu Ser Ser Leu Val Tyr Phe His Cys Ser Val 605 610 615	1875
TTA ATC TGC AGT CGA CTG TCT GCT GAC TCC CCT CTG TGT TCC GTG ACT Leu Ile Cys Ser Arg Leu Ser Ala Asp Ser Pro Leu Cys Ser Val Thr 620 625 630	1923
TGC CCT GTG TCA TTC AGA CAC AGG AGA GCC ACA GGC ACC ACT GAA GAA Cys Pro Val Ser Phe Arg His Arg Arg Ala Thr Gly Thr Thr Glu Glu 635 640 645	1971
GAG AAA ATG ATA GTG AGT CTT CCA GGA CCC ATC CTC CTG CTG TCA GAT Glu Lys Met Ile Val Ser Leu Pro Gly Pro Ile Leu Leu Leu Ser Asp 650 655 660	2019
AGC TCT TCA CTC AGA GAT GTG GTG GAC TCA AAA GGG TAT GGG GCT GCC Ser Ser Ser Leu Arg Asp Val Val Asp Ser Lys Gly Tyr Gly Ala Ala 665 670 675 680	2067
GGA TAT GTT GCT TTT AAG ACT GTG GTA GCT GTG GCT GCC TTA GCA GGC Gly Tyr Val Ala Phe Lys Thr Val Val Ala Val Ala Ala Leu Ala Gly 685 690 695	2115
CTC GTG GCA ACG CTA GGC TTC ATC ACC TAC CTG CGC AAG AAC AGA ACC Leu Val Ala Thr Leu Gly Phe Ile Thr Tyr Leu Arg Lys Asn Arg Thr 700 705 710	2163
ATG ATA AAT CAC TAAGGATTTT CAAATAAAAT GGTGAAGTA AAAAAAAAAA Met Ile Asn His 715	2215
AAAAAAGCG GCCGCGAATT C	2236

(2) INFORMATION FOR SEQ ID NO:14:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Met Ala Ser Arg Gln Lys Gly Asp Ser Gly Ser Pro Ser Ser Trp Phe
 1           5           10           15
Asn Ala Asp Trp Ser Thr Tyr Arg Ser Leu Phe Leu Leu Phe Ile Leu
 20           25           30
Val Thr Ser Val Asn Ser Ile Gly Val Leu Gln Leu Val Asn Pro Val
 35           40           45
Phe Pro Gly Thr Val Thr Cys Tyr Glu Thr Arg Met Ala Val Glu Phe
 50           55           60
Pro Ser Asp Phe Gly Thr Lys Lys Trp His Thr Ser Val Val Asp Pro
 65           70           75           80
Phe Ser Phe Glu Leu Leu Asn Cys Thr Tyr Ile Leu Asp Pro Glu Asn
 85           90           95
Leu Thr Leu Lys Ala Pro Tyr Glu Thr Cys Thr Arg Arg Thr Leu Gly
100           105           110
Gln His Arg Met Ile Ile Arg Leu Lys Asp His Asn Ala Ala Ser Arg
115           120           125
His Asn Ser Leu Met Tyr Gln Ile Asn Cys Pro Val Met Gln Ala Glu
130           135           140
Glu Thr His Glu His Ala Gly Ser Thr Ile Cys Thr Lys Asp Ser Met
145           150           155           160
Ser Phe Thr Phe Asn Val Ile Pro Gly Leu Ala Asp Glu Asn Thr Asp
165           170           175
Ile Lys Asn Pro Met Gly Trp Ser Ile Glu Val Gly Asp Gly Thr Lys
180           185           190
Ala Lys Thr Leu Thr Leu Gln Asp Val Leu Arg Gln Gly Tyr Asn Ile
195           200           205
Leu Phe Asp Asn His Lys Ile Thr Phe Gln Val Ser Phe Asn Ala Thr
210           215           220
Gly Val Thr His Tyr Met Gln Gly Asn Ser His Leu Tyr Met Val Pro
225           230           235           240
Leu Lys Leu Ile His Glu Ser Leu Gly Gln Lys Ile Ile Leu Thr Thr
245           250           255
Arg Val Leu Cys Met Ser Asp Ala Val Thr Cys Asn Ala Thr His Val
260           265           270
Thr Leu Thr Ile Pro Glu Phe Pro Gly Lys Leu Lys Ser Val Ser Ser
275           280           285
Glu Asn Arg Asn Phe Ala Val Ser Gln Leu His Asn Asn Gly Ile Asp
290           295           300
Lys Glu Glu Ser Ser Gly Leu Thr Leu His Phe Ser Lys Thr Leu Leu

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305		310		315		320
Lys Met Glu Phe Ser 325	Glu Lys Cys Leu Pro 330	Tyr Gln Phe Tyr Leu Ala 335				
Ser Leu Lys Leu Thr 340	Phe Ala Phe Asn Gln Glu Thr Ile Ser Thr Val 350					
Leu Tyr Pro 355	Glu Cys Val Cys Glu Ser Pro Val Ser Ile Val Thr Gly 365					
Asp Leu Cys Thr Gln Asp 370	Gly Phe Met Asp Ile Lys Val Tyr Ser His 380					
Gln Thr Lys Pro Ala Leu 390	Asn Leu Glu Thr Leu Arg Val Gly Asp Ser 400					
Ser Cys Gln Pro Thr 405	Phe Gln Ala Ala Ser Gln Gly Leu Ile Leu Phe 415					
His Ile Pro Leu Asn Gly Cys Gly Thr Arg His Lys Phe Lys Glu Gly 420						
Lys Val Ile Tyr Glu Asn Glu Ile His Ala Val Trp Ala Asp Leu Pro 435						
Pro Ser Thr Ile Ser Arg Asp Ser Glu Phe Arg Met Thr Val Gln Cys 450						
His Tyr Ser Lys Gly Asp Leu Leu Ile Asn Thr Arg Val Gln Ser Leu 465						
Pro Pro Leu Glu Ala Ser Val Arg Pro Gly Pro Leu Ala Leu Ile Leu 485						
Gln Thr Tyr Pro Asp Lys Ser Tyr Leu Gln Pro Tyr Gly Glu Lys Glu 500						
Tyr Pro Val Val Arg Tyr Leu Arg Gln Pro Ile Tyr Leu Glu Val Arg 515						
Val Leu Asn Arg Ser Asp Pro Asn Ile Lys Leu Val Leu Asp Asp Cys 530						
Trp Ala Thr Pro Thr Met Asp Pro Ala Ser Val Pro Gln Trp Asn Ile 545						
Ile Met Asp Gly Cys Glu Tyr Asn Leu Asp Asn His Arg Thr Thr Phe 565						
His Pro Val Gly Ser Ser Val Thr Tyr Pro Thr His Tyr Arg Arg Phe 580						
Asp Val Lys Thr Phe Ala Phe Val Ser Glu Ala Gln Val Leu Ser Ser 595						
Leu Val Tyr Phe His Cys Ser Val Leu Ile Cys Ser Arg Leu Ser Ala 610						
Asp Ser Pro Leu Cys Ser Val Thr Cys Pro Val Ser Phe Arg His Arg 625						
Arg Ala Thr Gly Thr Thr Glu Glu Glu Lys Met Ile Val Ser Leu Pro 645						
Gly Pro Ile Leu Leu Leu Ser Asp Ser Ser Ser Leu Arg Asp Val Val 660						

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(2) INFORMATION FOR SEQ ID NO:15:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Felis domesticus*
(D) DEVELOPMENTAL STAGE: Juvenile
(E) HAPLOTYPE: Diploidy
(F) TISSUE TYPE: Ovary
(G) CELL TYPE: Oocyte

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 57..1766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGCG GCCGAAGTA CAGGTCCTGC AGCCAGTGGG GGCTCCCGAT GGCATC																56
ATG	TGG	CTG	CTG	CAG	CCC	CTC	TTG	CTC	TGT	GTT	CCC	TTG	TCT	CTC	GCT	104
Met	Trp	Leu	Leu	Gln	Pro	Leu	Leu	Leu	Cys	Val	Pro	Leu	Ser	Leu	Ala	
1				5					10					15		
GTG	CAT	GGC	CAG	CAG	AAG	CCC	CAG	GTA	CCA	GAT	TAT	CCC	GGT	GAA	CTC	152
Val	His	Gly	Gln	Gln	Lys	Pro	Gln	Val	Pro	Asp	Tyr	Pro	Gly	Glu	Leu	
			20					25					30			
CAT	TGT	GGG	CTC	CAG	AGC	CTT	CAG	TTT	GCC	ATA	AAC	CCG	AGC	CCC	GGG	200
His	Cys	Gly	Leu	Gln	Ser	Leu	Gln	Phe	Ala	Ile	Asn	Pro	Ser	Pro	Gly	
		35					40					45				
AAA	GCG	ACT	CCT	GCA	CTC	ATA	GTC	TGG	GAC	AAT	CGC	GGG	CTG	CCA	CAC	248
Lys	Ala	Thr	Pro	Ala	Leu	Ile	Val	Trp	Asp	Asn	Arg	Gly	Leu	Pro	His	
	50					55					60					
AAG	CTG	CAG	AAC	AAC	TCT	GGC	TGC	GGT	ACC	TGG	GTA	AGG	GAG	AGC	CCG	296
Lys	Leu	Gln	Asn	Asn	Ser	Gly	Cys	Gly	Thr	Trp	Val	Arg	Glu	Ser	Pro	
65					70					75					80	
GGG	GGC	TCC	GTG	CTG	TTA	GAC	GCC	TCT	TAC	AGC	AGC	TGC	TAT	GTC	AAC	344
Gly	Gly	Ser	Val	Leu	Leu	Asp	Ala	Ser	Tyr	Ser	Ser	Cys	Tyr	Val	Asn	
				85					90					95		
GAG	TGG	GTG	AGC	ACG	ACC	CAA	TCC	CCA	GGA	ACG	TCG	AGG	CCC	CCC	ACC	392
Glu	Trp	Val	Ser	Thr	Thr	Gln	Ser	Pro	Gly	Thr	Ser	Arg	Pro	Pro	Thr	
			100					105					110			

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CCA GCA TCC AGG GTG ACT CCC CAG GAC TCC CAC TAC GTC ATG ATA GTC Pro Ala Ser Arg Val Thr Pro Gln Asp Ser His Tyr Val Met Ile Val 115 120 125	440
GGA GTT GAA GGC ACA GAT GCG GCT GGG CGC AGG GTT ACC AAC ACC AAG Gly Val Glu Gly Thr Asp Ala Ala Gly Arg Arg Val Thr Asn Thr Lys 130 135 140	488
GTG CTC AGG TGT CCT AGG AAT CCC CCA GAC CAA GCT TTG GTG TCG AGC Val Leu Arg Cys Pro Arg Asn Pro Pro Asp Gln Ala Leu Val Ser Ser 145 150 155 160	536
TTA AGT CCC TCT CCT CTT CAA AAC GTA GCA CTA GAA GCT CCA AAC GCT Leu Ser Pro Ser Pro Leu Gln Asn Val Ala Leu Glu Ala Pro Asn Ala 165 170 175	584
GAC TTG TGT GAC TCT GTC CCA AAG TGG GAC AGG CTT CCG TGT GCT TCT Asp Leu Cys Asp Ser Val Pro Lys Trp Asp Arg Leu Pro Cys Ala Ser 180 185 190	632
TCA CCC ATC ACT CAG GGA GAC TGC AAT AAG CTT GGT TGC TGC TAC AAA Ser Pro Ile Thr Gln Gly Asp Cys Asn Lys Leu Gly Cys Cys Tyr Lys 195 200 205	680
TCA GAG GCA AAT TCC TGT TAC TAT GGA AAC ACA GTG ACC TCA CGC TGT Ser Glu Ala Asn Ser Cys Tyr Tyr Gly Asn Thr Val Thr Ser Arg Cys 210 215 220	728
ACC CAA GAC GGC CAC TTC TCC ATC GCC GTG TCT CGG AAC GTG ACC TCA Thr Gln Asp Gly His Phe Ser Ile Ala Val Ser Arg Asn Val Thr Ser 225 230 235 240	776
CCC CCA CTG CTC TTA AAT TCT CTG CGC TTG GCC TTC GGG AAG GAC CGC Pro Pro Leu Leu Leu Asn Ser Leu Arg Leu Ala Phe Gly Lys Asp Arg 245 250 255	824
GAA TGT AAC CCT GTG AAA GCA ACA CGT GCC TTT GCC CTG TTC TTT TTT Glu Cys Asn Pro Val Lys Ala Thr Arg Ala Phe Ala Leu Phe Phe Phe 260 265 270	872
CCA TTT AAT TCC TGT GGC ACC ACG AGA TGG GTC ACT GGA GAC CAG GCA Pro Phe Asn Ser Cys Gly Thr Thr Arg Trp Val Thr Gly Asp Gln Ala 275 280 285	920
GTA TAT GAA AAT GAG CTG GTG GCA GCT AGA GAT GTG AGA ACT TGG AGC Val Tyr Glu Asn Glu Leu Val Ala Ala Arg Asp Val Arg Thr Trp Ser 290 295 300	968
CAT GGT TCT ATT ACC CGT GAC AGT ATC TTC AGG CTT CGA GTT AGC TGC His Gly Ser Ile Thr Arg Asp Ser Ile Phe Arg Leu Arg Val Ser Cys 305 310 315 320	1016
AGC TAC TCT GTA AGG AGT AAT GCC TTC CCG CTT AGC GTT CAG GTG TTT Ser Tyr Ser Val Arg Ser Asn Ala Phe Pro Leu Ser Val Gln Val Phe 325 330 335	1064
ACC ATC CCA CCA CCC CAT CTG AAA ACC CAG CAT GGA CCC CTC ACT CTG Thr Ile Pro Pro Pro His Leu Lys Thr Gln His Gly Pro Leu Thr Leu 340 345 350	1112
GAA CTC AAG ATT GCC AAA GAT AAG CAC TAT GGC TCC TAC TAC ACT ATT Glu Leu Lys Ile Ala Lys Asp Lys His Tyr Gly Ser Tyr Tyr Thr Ile 355 360 365	1160
GGT GAC TAC CCA GTG GTA AAG TTG CTT CGG GAT CCC ATT TAT GTG GAG Gly Asp Tyr Pro Val Val Lys Leu Leu Arg Asp Pro Ile Tyr Val Glu 370 375 380	1208

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GTC TCT ATC CGC CAC AGA ACG GAC CCC TCC CTG GGG CTG CTC CTC CAT Val Ser Ile Arg His Arg Thr Asp Pro Ser Leu Gly Leu Leu Leu His 385 390 395 400	1256
AAC TGT TGG GCC ACA CCC GGC AAG AAC TCC CAG AGT CTG TCC CAG TGG Asn Cys Trp Ala Thr Pro Gly Lys Asn Ser Gln Ser Leu Ser Gln Trp 405 410 415	1304
CCC ATT CTG GTG AAA GGA TGC CCC TAC GTT GGA GAC AAC TAT CAA ACC Pro Ile Leu Val Lys Gly Cys Pro Tyr Val Gly Asp Asn Tyr Gln Thr 420 425 430	1352
CAG CTG ATC CCT GTC CAG AAG GCT CTG GAT ACA CCA TTT CCA TCT TAC Gln Leu Ile Pro Val Gln Lys Ala Leu Asp Thr Pro Phe Pro Ser Tyr 435 440 445	1400
TAC AAG CGC TTC AGT ATT TTC ACC TTC AGC TTT GTG GAC ACC ATG GCA Tyr Lys Arg Phe Ser Ile Phe Thr Phe Ser Phe Val Asp Thr Met Ala 450 455 460	1448
AAG TGG GCA CTC AGG GGA CCG GTG TAT CTG CAC TGT AAT GTA TCC ATC Lys Trp Ala Leu Arg Gly Pro Val Tyr Leu His Cys Asn Val Ser Ile 465 470 475 480	1496
TGC CAG CCT GCT GGG ACC TCC TCC TGT AGG ATA ACC TGT CCT GTT GCC Cys Gln Pro Ala Gly Thr Ser Ser Cys Arg Ile Thr Cys Pro Val Ala 485 490 495	1544
AGG CGA AGA AGA CAC TCT GAC CTC CAT CAT CAC AGC AGT ACT GCG AGC Arg Arg Arg Arg His Ser Asp Leu His His His Ser Ser Thr Ala Ser 500 505 510	1592
ATC TCT AGC AAG GGT CCC ATG ATT CTA CTC CAA GCC ACT ATG GAC TCT Ile Ser Ser Lys Gly Pro Met Ile Leu Leu Gln Ala Thr Met Asp Ser 515 520 525	1640
GCA GAG AAG CTC CAC AAA AAC TCA AGT TCT CCT ATA GAC TCC CAA GCT Ala Glu Lys Leu His Lys Asn Ser Ser Ser Pro Ile Asp Ser Gln Ala 530 535 540	1688
CTG TGG ATG GCA GGC CTT TCC GGG ACC CTA ATC TTT GGA TTC TTG TTA Leu Trp Met Ala Gly Leu Ser Gly Thr Leu Ile Phe Gly Phe Leu Leu 545 550 555 560	1736
GTG TCC TAC TTG GCT ATC AGG AAA CGG AGG TGAATTATTC CAGTTGTGTT Val Ser Tyr Leu Ala Ile Arg Lys Arg Arg 565 570	1786
AATAAAACCA GATTGCATTA CCAAAAAAAA AAAAAAAA GCGGCCGCGA ATTC	1840

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Trp Leu Leu Gln Pro Leu Leu Leu Cys Val Pro Leu Ser Leu Ala	
1 5 10 15	
Val His Gly Gln Gln Lys Pro Gln Val Pro Asp Tyr Pro Gly Glu Leu	
20 25 30	

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His Cys Gly Leu Gln Ser Leu Gln Phe Ala Ile Asn Pro Ser Pro Gly
 35 40 45
 Lys Ala Thr Pro Ala Leu Ile Val Trp Asp Asn Arg Gly Leu Pro His
 50 55 60
 Lys Leu Gln Asn Asn Ser Gly Cys Gly Thr Trp Val Arg Glu Ser Pro
 65 70 75 80
 Gly Gly Ser Val Leu Leu Asp Ala Ser Tyr Ser Ser Cys Tyr Val Asn
 85 90 95
 Glu Trp Val Ser Thr Thr Gln Ser Pro Gly Thr Ser Arg Pro Pro Thr
 100 105 110
 Pro Ala Ser Arg Val Thr Pro Gln Asp Ser His Tyr Val Met Ile Val
 115 120 125
 Gly Val Glu Gly Thr Asp Ala Ala Gly Arg Arg Val Thr Asn Thr Lys
 130 135 140
 Val Leu Arg Cys Pro Arg Asn Pro Pro Asp Gln Ala Leu Val Ser Ser
 145 150 155 160
 Leu Ser Pro Ser Pro Leu Gln Asn Val Ala Leu Glu Ala Pro Asn Ala
 165 170 175
 Asp Leu Cys Asp Ser Val Pro Lys Trp Asp Arg Leu Pro Cys Ala Ser
 180 185 190
 Ser Pro Ile Thr Gln Gly Asp Cys Asn Lys Leu Gly Cys Cys Tyr Lys
 195 200 205
 Ser Glu Ala Asn Ser Cys Tyr Tyr Gly Asn Thr Val Thr Ser Arg Cys
 210 215 220
 Thr Gln Asp Gly His Phe Ser Ile Ala Val Ser Arg Asn Val Thr Ser
 225 230 235 240
 Pro Pro Leu Leu Leu Asn Ser Leu Arg Leu Ala Phe Gly Lys Asp Arg
 245 250 255
 Glu Cys Asn Pro Val Lys Ala Thr Arg Ala Phe Ala Leu Phe Phe Phe
 260 265 270
 Pro Phe Asn Ser Cys Gly Thr Thr Arg Trp Val Thr Gly Asp Gln Ala
 275 280 285
 Val Tyr Glu Asn Glu Leu Val Ala Ala Arg Asp Val Arg Thr Trp Ser
 290 295 300
 His Gly Ser Ile Thr Arg Asp Ser Ile Phe Arg Leu Arg Val Ser Cys
 305 310 315 320
 Ser Tyr Ser Val Arg Ser Asn Ala Phe Pro Leu Ser Val Gln Val Phe
 325 330 335
 Thr Ile Pro Pro Pro His Leu Lys Thr Gln His Gly Pro Leu Thr Leu
 340 345 350
 Glu Leu Lys Ile Ala Lys Asp Lys His Tyr Gly Ser Tyr Tyr Thr Ile
 355 360 365
 Gly Asp Tyr Pro Val Val Lys Leu Leu Arg Asp Pro Ile Tyr Val Glu
 370 375 380
 Val Ser Ile Arg His Arg Thr Asp Pro Ser Leu Gly Leu Leu Leu His

385					390					395					400				
Asn	Cys	Trp	Ala	Thr	Pro	Gly	Lys	Asn	Ser	Gln	Ser	Leu	Ser	Gln	Trp				
				405					410					415					
Pro	Ile	Leu	Val	Lys	Gly	Cys	Pro	Tyr	Val	Gly	Asp	Asn	Tyr	Gln	Thr				
			420					425					430						
Gln	Leu	Ile	Pro	Val	Gln	Lys	Ala	Leu	Asp	Thr	Pro	Phe	Pro	Ser	Tyr				
		435					440					445							
Tyr	Lys	Arg	Phe	Ser	Ile	Phe	Thr	Phe	Ser	Phe	Val	Asp	Thr	Met	Ala				
	450					455					460								
Lys	Trp	Ala	Leu	Arg	Gly	Pro	Val	Tyr	Leu	His	Cys	Asn	Val	Ser	Ile				
	465					470					475				480				
Cys	Gln	Pro	Ala	Gly	Thr	Ser	Ser	Cys	Arg	Ile	Thr	Cys	Pro	Val	Ala				
				485					490					495					
Arg	Arg	Arg	Arg	His	Ser	Asp	Leu	His	His	His	Ser	Ser	Thr	Ala	Ser				
				500				505					510						
Ile	Ser	Ser	Lys	Gly	Pro	Met	Ile	Leu	Leu	Gln	Ala	Thr	Met	Asp	Ser				
		515					520					525							
Ala	Glu	Lys	Leu	His	Lys	Asn	Ser	Ser	Ser	Pro	Ile	Asp	Ser	Gln	Ala				
	530					535					540								
Leu	Trp	Met	Ala	Gly	Leu	Ser	Gly	Thr	Leu	Ile	Phe	Gly	Phe	Leu	Leu				
	545					550					555							560	
Val	Ser	Tyr	Leu	Ala	Ile	Arg	Lys	Arg	Arg										
				565					570										

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

ORIGINAL SOURCE:
(A) ORGANISM: *Felis domesticus*
(D) DEVELOPMENTAL STAGE: Juvenile
(E) HAPLOTYPE: Diploidy
(F) TISSUE TYPE: Ovary
(G) CELL TYPE: Oocyte

(ix) **FEATURE:**

(A) NAME/KEY: CDS
(B) LOCATION: 26..1297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGCGG CCGCGCGTAG GCCGC ATG GGG CTG AGC TAC GGG CTT TTC ATC
Met Gly Leu Ser Tyr Gly Leu Phe Ile
1 5

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TGT TTT CTG CTT TGG GCA GGC ACG GGG CTG TGC TAT CCC CCA ACC ACC Cys Phe Leu Leu Trp Ala Gly Thr Gly Leu Cys Tyr Pro Pro Thr Thr 10 15 20 25	100
ACC GAG GAT AAG ACC CAC CCC TCG TTG CCA TCA AGC CCC TCT GTG GTG Thr Glu Asp Lys Thr His Pro Ser Leu Pro Ser Ser Pro Ser Val Val 30 35 40	148
GTA GAG TGT CGG CAT GCC TGG CTG GTG GTC AAC GTC AGC AAA AAC CTT Val Glu Cys Arg His Ala Trp Leu Val Val Asn Val Ser Lys Asn Leu 45 50 55	196
TTT GGT ACT GGG AGG CTT GTG AGG CCT GCA GAC CTC ACC CTG GGT CCG Phe Gly Thr Gly Arg Leu Val Arg Pro Ala Asp Leu Thr Leu Gly Pro 60 65 70	244
GAG AAC TGT GAG CCC CTG ATC TCT GGG GAC TCA GAT GAT ACG GTC AGG Glu Asn Cys Glu Pro Leu Ile Ser Gly Asp Ser Asp Asp Thr Val Arg 75 80 85	292
TTT GAA GTC GAG CTC CAC AAG TGT GGC AAC AGC GTG CAG GTG ACC GAA Phe Glu Val Glu Leu His Lys Cys Gly Asn Ser Val Gln Val Thr Glu 90 95 100 105	340
GAT GCC CTG GTG TAT AGC ACC TTC CTG CTC CAC AAC CCC CGC CCC ATG Asp Ala Leu Val Tyr Ser Thr Phe Leu Leu His Asn Pro Arg Pro Met 110 115 120	388
GGA AAC CTG TCC ATC CTG AGG ACC AAC CGC GCG GAA GTT CCC ATT GAG Gly Asn Leu Ser Ile Leu Arg Thr Asn Arg Ala Glu Val Pro Ile Glu 125 130 135	436
TGC CGT TAC CCC AGG CAT AGC AAC GTG AGC AGC GAG GCC ATC CTG CCC Cys Arg Tyr Pro Arg His Ser Asn Val Ser Ser Glu Ala Ile Leu Pro 140 145 150	484
ACC TGG GTG CCC TTC AGG ACC ACA ATG CTC TCA GAG GAG AAG CTG GCT Thr Trp Val Pro Phe Arg Thr Thr Met Leu Ser Glu Glu Lys Leu Ala 155 160 165	532
TTC TCT CTG CGC CTG ATG GAG GAG GAC TGG GGC TCC GAG AAG CAG TCC Phe Ser Leu Arg Leu Met Glu Glu Asp Trp Gly Ser Glu Lys Gln Ser 170 175 180 185	580
CCC ACT TTC CAG TTG GGA GAC CTA GCC CAC CTC CAG GCC GAA GTC CAC Pro Thr Phe Gln Leu Gly Asp Leu Ala His Leu Gln Ala Glu Val His 190 195 200	628
ACC GGC CGC CAC ATA CCA CTG CGA CTG TTT GTG GAC TAC TGT GTG GCC Thr Gly Arg His Ile Pro Leu Arg Leu Phe Val Asp Tyr Cys Val Ala 205 210 215	676
ACG CTG ACA CCA GAC CAG AAC GCC TCC CCT CAT CAC ACC ATC GTG GAC Thr Leu Thr Pro Asp Gln Asn Ala Ser Pro His His Thr Ile Val Asp 220 225 230	724
TTC CAC GGC TGT CTC GTG GAT GGT CTC TCT GAT GCC TCT TCT GCC TTC Phe His Gly Cys Leu Val Asp Gly Leu Ser Asp Ala Ser Ser Ala Phe 235 240 245	772
AAA GCC CCC AGA CCC AGG CCG GAG ACT CTC CAG TTT ACA GTA GAC ACG Lys Ala Pro Arg Pro Arg Pro Glu Thr Leu Gln Phe Thr Val Asp Thr 250 255 260 265	820
TTC CAC TTT GCT AAT GAC CCC AGA AAC ATG ATC TAT ATC ACC TGC CAT Phe His Phe Ala Asn Asp Pro Arg Asn Met Ile Tyr Ile Thr Cys His 270 275 280	868

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CTG AAA GTC ACT CCA GCT AGC CGA GTC CCA GAC CAG CTA AAC AAA GCC Leu Lys Val Thr Pro Ala Ser Arg Val Pro Asp Gln Leu Asn Lys Ala 285 290 295	916
TGT TCC TTC ATC AAG TCT TCT AAC AGG TGG TTC CCA GTA GAA GGC CCT Cys Ser Phe Ile Lys Ser Ser Asn Arg Trp Phe Pro Val Glu Gly Pro 300 305 310	964
GCT GAC ATC TGT AAC TGT TGT AAC AAA GGT AGC TGT GGC CTT CAG GGC Ala Asp Ile Cys Asn Cys Cys Asn Lys Gly Ser Cys Gly Leu Gln Gly 315 320 325	1012
CGT TCC TGG AGG CTG TCC CAC CTA GAC AGA CCG TGG CAC AAG ATG GCT Arg Ser Trp Arg Leu Ser His Leu Asp Arg Pro Trp His Lys Met Ala 330 335 340 345	1060
TCC CGA AAT CGC AGG CAT GTG ACC GAA GAA GCG GAT ATC ACC GTG GGG Ser Arg Asn Arg Arg His Val Thr Glu Ala Asp Ile Thr Val Gly 350 355 360	1108
CCT CTG ATC TTC CTG GGA AAG GCT GCC GAT CGT GGT GTG GAG GGG TCG Pro Leu Ile Phe Leu Gly Lys Ala Ala Asp Arg Gly Val Glu Gly Ser 365 370 375	1156
ACC TCG CCT CAC ACC TCT GTG ATG GTG GGC ATA GGC CTG GCC ACG GTG Thr Ser Pro His Thr Ser Val Met Val Gly Ile Gly Leu Ala Thr Val 380 385 390	1204
TTG TCC CTG ACT CTG GCT ACC ATT GTC CTG GGT CTC GCC AGG AGG CAT Leu Ser Leu Thr Leu Ala Thr Ile Val Leu Gly Leu Ala Arg Arg His 395 400 405	1252
CAC ACT GCT TCC CGT CCT ATG ATC TGC CCT GTG TCT GCT TCC CAA His Thr Ala Ser Arg Pro Met Ile Cys Pro Val Ser Ala Ser Gln 410 415 420	1297
TAAAGAAGC GGCCGCGAAT TC	1319

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 424 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Gly Leu Ser Tyr Gly Leu Phe Ile Cys Phe Leu Leu Trp Ala Gly 1 5 10 15
Thr Gly Leu Cys Tyr Pro Pro Thr Thr Thr Glu Asp Lys Thr His Pro 20 25 30
Ser Leu Pro Ser Ser Pro Ser Val Val Val Glu Cys Arg His Ala Trp 35 40 45
Leu Val Val Asn Val Ser Lys Asn Leu Phe Gly Thr Gly Arg Leu Val 50 55 60
Arg Pro Ala Asp Leu Thr Leu Gly Pro Glu Asn Cys Glu Pro Leu Ile 65 70 75 80
Ser Gly Asp Ser Asp Asp Thr Val Arg Phe Glu Val Glu Leu His Lys 85 90 95

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Cys Gly Asn Ser Val Gln Val Thr Glu Asp Ala Leu Val Tyr Ser Thr
 100 105 110
 Phe Leu Leu His Asn Pro Arg Pro Met Gly Asn Leu Ser Ile Leu Arg
 115 120 125
 Thr Asn Arg Ala Glu Val Pro Ile Glu Cys Arg Tyr Pro Arg His Ser
 130 135 140
 Asn Val Ser Ser Glu Ala Ile Leu Pro Thr Trp Val Pro Phe Arg Thr
 145 150 155 160
 Thr Met Leu Ser Glu Glu Lys Leu Ala Phe Ser Leu Arg Leu Met Glu
 165 170 175
 Glu Asp Trp Gly Ser Glu Lys Gln Ser Pro Thr Phe Gln Leu Gly Asp
 180 185 190
 Leu Ala His Leu Gln Ala Glu Val His Thr Gly Arg His Ile Pro Leu
 195 200 205
 Arg Leu Phe Val Asp Tyr Cys Val Ala Thr Leu Thr Pro Asp Gln Asn
 210 215 220
 Ala Ser Pro His His Thr Ile Val Asp Phe His Gly Cys Leu Val Asp
 225 230 235 240
 Gly Leu Ser Asp Ala Ser Ser Ala Phe Lys Ala Pro Arg Pro Arg Pro
 245 250 255
 Glu Thr Leu Gln Phe Thr Val Asp Thr Phe His Phe Ala Asn Asp Pro
 260 265 270
 Arg Asn Met Ile Tyr Ile Thr Cys His Leu Lys Val Thr Pro Ala Ser
 275 280 285
 Arg Val Pro Asp Gln Leu Asn Lys Ala Cys Ser Phe Ile Lys Ser Ser
 290 295 300
 Asn Arg Trp Phe Pro Val Glu Gly Pro Ala Asp Ile Cys Asn Cys Cys
 305 310 315 320
 Asn Lys Gly Ser Cys Gly Leu Gln Gly Arg Ser Trp Arg Leu Ser His
 325 330 335
 Leu Asp Arg Pro Trp His Lys Met Ala Ser Arg Asn Arg Arg His Val
 340 345 350
 Thr Glu Glu Ala Asp Ile Thr Val Gly Pro Leu Ile Phe Leu Gly Lys
 355 360 365
 Ala Ala Asp Arg Gly Val Glu Gly Ser Thr Ser Pro His Thr Ser Val
 370 375 380
 Met Val Gly Ile Gly Leu Ala Thr Val Leu Ser Leu Thr Leu Ala Thr
 385 390 395 400
 Ile Val Leu Gly Leu Ala Arg Arg His His Thr Ala Ser Arg Pro Met
 405 410 415
 Ile Cys Pro Val Ser Ala Ser Gln
 420

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bos taurus
 (D) DEVELOPMENTAL STAGE: Juvenile
 (E) HAPLOTYPE: Diploidy
 (F) TISSUE TYPE: Ovary
 (G) CELL TYPE: Oocyte

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 16..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGCGG CCGCC CTA AAC AGG ACT GAC CCC AAC ATC AAG TTG GTC TTA	51
Leu Asn Arg Thr Asp Pro Asn Ile Lys Leu Val Leu	
1 5 10	
GAT GAT TGC TGG GCA ACA TCC ACC ATG GAC CCA GCC TCT CTC CCT CAG	99
Asp Asp Cys Trp Ala Thr Ser Thr Met Asp Pro Ala Ser Leu Pro Gln	
15 20 25	
TGG AAT ATT ATC GTG GAT GGC TGT GAA TAC AAC TTG GAC AAC CAC AGA	147
Trp Asn Ile Ile Val Asp Gly Cys Glu Tyr Asn Leu Asp Asn His Arg	
30 35 40	
ACC ACC TTC CAT CCG GTT GGC TCC TCG GTG GCC TAT CCT AAT CAC TAC	195
Thr Thr Phe His Pro Val Gly Ser Ser Val Ala Tyr Pro Asn His Tyr	
45 50 55 60	
CAG AGG TTT GCT GTG AAG ACC TTT GCC TTT GTG TCA GAG GAC CCG GCG	243
Gln Arg Phe Ala Val Lys Thr Phe Ala Phe Val Ser Glu Asp Pro Ala	
65 70 75	
TTC TCT CAC TTG GTC TAC TTC CAC TGC AGC GCC TTA ATC TGC GAT CAA	291
Phe Ser His Leu Val Tyr Phe His Cys Ser Ala Leu Ile Cys Asp Gln	
80 85 90	
CTT TCT TCT AAC TTC CCC CTG TGT TCT GCG TCT TGC CTT GTG TCA TCC	339
Leu Ser Ser Asn Phe Pro Leu Cys Ser Ala Ser Cys Leu Val Ser Ser	
95 100 105	
AGA AGC AGG CGA GCC ACA GGG GCC ACT GAG GAA GAG AAG ATG ATA GTG	387
Arg Ser Arg Arg Ala Thr Gly Ala Thr Glu Glu Glu Lys Met Ile Val	
110 115 120	
AGT CTC CCG GGC CCC ATC CTC CTG TTG TCA GAT GGC TCT TCA TTC AGA	435
Ser Leu Pro Gly Pro Ile Leu Leu Leu Ser Asp Gly Ser Ser Phe Arg	
125 130 135 140	
GAT GCT GTG GAT TCT AAA GGG CAT GGG ACT TCT GGA TAT GCT GCT TTT	483
Asp Ala Val Asp Ser Lys Gly His Gly Thr Ser Gly Tyr Ala Ala Phe	
145 150 155	
AAA ACT ATG GTT GCT GTA GTT GCC TTA GCA GGT GTT GTG GCA ACT CTA	531
Lys Thr Met Val Ala Val Val Ala Leu Ala Gly Val Val Ala Thr Leu	
160 165 170	

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AGC CTA ATC AGC TAC CTG CGC AAG AAA AGA ATC ACA GTG CTA AAC CAC 579
 Ser Leu Ile Ser Tyr Leu Arg Lys Lys Arg Ile Thr Val Leu Asn His
 175 180 185
 TAATTGGATT TTCAATAAAA TGTGGAAGTA AAAAAAAAAA AAAAAAAAAA GCGGCCCGCA 639
 ATTC 643

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Asn Arg Thr Asp Pro Asn Ile Lys Leu Val Leu Asp Asp Cys Trp
 1 5 10 15
 Ala Thr Ser Thr Met Asp Pro Ala Ser Leu Pro Gln Trp Asn Ile Ile
 20 25 30
 Val Asp Gly Cys Glu Tyr Asn Leu Asp Asn His Arg Thr Thr Phe His
 35 40 45
 Pro Val Gly Ser Ser Val Ala Tyr Pro Asn His Tyr Gln Arg Phe Ala
 50 55 60
 Val Lys Thr Phe Ala Phe Val Ser Glu Asp Pro Ala Phe Ser His Leu
 65 70 75 80
 Val Tyr Phe His Cys Ser Ala Leu Ile Cys Asp Gln Leu Ser Ser Asn
 85 90 95
 Phe Pro Leu Cys Ser Ala Ser Cys Leu Val Ser Ser Arg Ser Arg Arg
 100 105 110
 Ala Thr Gly Ala Thr Glu Glu Glu Lys Met Ile Val Ser Leu Pro Gly
 115 120 125
 Pro Ile Leu Leu Leu Ser Asp Gly Ser Ser Phe Arg Asp Ala Val Asp
 130 135 140
 Ser Lys Gly His Gly Thr Ser Gly Tyr Ala Ala Phe Lys Thr Met Val
 145 150 155 160
 Ala Val Val Ala Leu Ala Gly Val Val Ala Thr Leu Ser Leu Ile Ser
 165 170 175
 Tyr Leu Arg Lys Lys Arg Ile Thr Val Leu Asn His
 180 185

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1029 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bos taurus
- (D) DEVELOPMENTAL STAGE: Juvenile
- (E) HAPLOTYPE: Diploidy
- (F) TISSUE TYPE: Ovary
- (G) CELL TYPE: Oocyte

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

G AAT TCT GTA CAC TTG GCC TTC AGG AAT GAC AGC GAA TGT AAA CCT	46
Asn Ser Val His Leu Ala Phe Arg Asn Asp Ser Glu Cys Lys Pro	
1 5 10 15	
GTG ATG GCA ACA CAC ACT TTT GTT CTG TTC CGG TTT CCA TTT ACT ACT	94
Val Met Ala Thr His Thr Phe Val Leu Phe Arg Phe Pro Phe Thr Thr	
20 25 30	
TGT GGT ACT ACA AAA CAG ATC ACT GGA AAG CAA GCG GTA TAT GAA AAT	142
Cys Gly Thr Thr Lys Gln Ile Thr Gly Lys Gln Ala Val Tyr Glu Asn	
35 40 45	
GAG CTG GTT GCA GCT CGG GAT GTG AGA ACT TGG AGC CGT GGT TCT ATT	190
Glu Leu Val Ala Ala Arg Asp Val Arg Thr Trp Ser Arg Gly Ser Ile	
50 55 60	
ACC CGA GAC AGT ACC TTC AGG CTC CAA GTC AGT TGT AGC TAC TCT GCA	238
Thr Arg Asp Ser Thr Phe Arg Leu Gln Val Ser Cys Ser Tyr Ser Ala	
65 70 75	
AGT AGC AGT GCT CTC CCA GTT AAT GTC CAA GTT CTT ACT CTC CCA CCA	286
Ser Ser Ser Ala Leu Pro Val Asn Val Gln Val Leu Thr Leu Pro Pro	
80 85 90 95	
CCC CTT CCT GAG ACC CTG CCT GGA AAC CTC ACT CTG GAA CTT AAG ATT	334
Pro Leu Pro Glu Thr Leu Pro Gly Asn Leu Thr Leu Glu Leu Lys Ile	
100 105 110	
GCC AAA GAT AAA CCG TAT CGC TCC TAC TAC ACG GCT AGT GAC TAC CCA	382
Ala Lys Asp Lys Pro Tyr Arg Ser Tyr Tyr Thr Ala Ser Asp Tyr Pro	
115 120 125	
GTG GTG AAG TTA CTT CGG GAT CCC ATC TAC GTG GAA GTC TCC ATC CAT	430
Val Val Lys Leu Leu Arg Asp Pro Ile Tyr Val Glu Val Ser Ile His	
130 135 140	
CAG AGA ACA GAC CCC AGT CTC GAG CTG CGC CTG GAC CAG TGT TGG GCG	478
Gln Arg Thr Asp Pro Ser Leu Glu Leu Arg Leu Asp Gln Cys Trp Ala	
145 150 155	
ACA CCT GGT GCA GAT GCC CTG CTC CAG CCC CAG TGG CCC TTG CTT GTG	526
Thr Pro Gly Ala Asp Ala Leu Leu Gln Pro Gln Trp Pro Leu Leu Val	
160 165 170 175	
AAT GGG TGC CCC TAC ACA GGA GAC AAC TAT CAG ACA AAA CTG ATC CCT	574
Asn Gly Cys Pro Tyr Thr Gly Asp Asn Tyr Gln Thr Lys Leu Ile Pro	
180 185 190	

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GTC TGG GAA GCC TCA GAC CTG CCG TTT CCT TCT CAC TAC CAG CGC TTC Val Trp Glu Ala Ser Asp Leu Pro Phe Pro Ser His Tyr Gln Arg Phe 195 200 205	622
AGC ATT TCC ACC TTC AGC TTT GTG GAC TCA GTG GCA AAG CGG GCC CTC Ser Ile Ser Thr Phe Ser Phe Val Asp Ser Val Ala Lys Arg Ala Leu 210 215 220	670
AAG GGA CCG GTG TAT CTG CAC TGC AGT GCA TCG GTC TGC CAG CCT GCC Lys Gly Pro Val Tyr Leu His Cys Ser Ala Ser Val Cys Gln Pro Ala 225 230 235	718
GGG ACA CCA TCC TGT GTG ACA CTC TGT CCT GCC AGA CGA AGA AGA AGC Gly Thr Pro Ser Cys Val Thr Leu Cys Pro Ala Arg Arg Arg Arg Ser 240 245 250 255	766
TCT GAC ATC CAT TTT CAG AAC AAA ACG GCT AGC ATT TCT AGC AAG GGT Ser Asp Ile His Phe Gln Asn Lys Thr Ala Ser Ile Ser Ser Lys Gly 260 265 270	814
CCC TTG ATT CTA CTC CAA GCC ATT CAA GAC TCT TCA GAA AAG CTC CAC Pro Leu Ile Leu Gln Ala Ile Gln Asp Ser Ser Glu Lys Leu His 275 280 285	862
AAA TAC TCA AGG TCT CCT GTA GAC TCT CAA GCT TTG TGG GTG GCT GGC Lys Tyr Ser Arg Ser Pro Val Asp Ser Gln Ala Leu Trp Val Ala Gly 290 295 300	910
CTA TCT GGA ATC TTA ATC GTT GGA GCC TTG TTC ATG TCC TAC CTG GCC Leu Ser Gly Ile Leu Ile Val Gly Ala Leu Phe Met Ser Tyr Leu Ala 305 310 315	958
ATT AGG AAA TGG AGA TGAGTTGCTC AGCCCAATG TGTTAATAAA ACCAGATTGC Ile Arg Lys Trp Arg 320	1013
AGCCGGCCGC GAATTC	1029

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asn Ser Val His Leu Ala Phe Arg Asn Asp Ser Glu Cys Lys Pro Val 1 5 10 15
Met Ala Thr His Thr Phe Val Leu Phe Arg Phe Pro Phe Thr Thr Cys 20 25 30
Gly Thr Thr Lys Gln Ile Thr Gly Lys Gln Ala Val Tyr Glu Asn Glu 35 40 45
Leu Val Ala Ala Arg Asp Val Arg Thr Trp Ser Arg Gly Ser Ile Thr 50 55 60
Arg Asp Ser Thr Phe Arg Leu Gln Val Ser Cys Ser Tyr Ser Ala Ser 65 70 75 80
Ser Ser Ala Leu Pro Val Asn Val Gln Val Leu Thr Leu Pro Pro Pro 85 90 95

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Leu Pro Glu Thr Leu Pro Gly Asn Leu Thr Leu Glu Leu Lys Ile Ala
 100 105 110
 Lys Asp Lys Pro Tyr Arg Ser Tyr Tyr Thr Ala Ser Asp Tyr Pro Val
 115 120 125
 Val Lys Leu Leu Arg Asp Pro Ile Tyr Val Glu Val Ser Ile His Gln
 130 135 140
 Arg Thr Asp Pro Ser Leu Glu Leu Arg Leu Asp Gln Cys Trp Ala Thr
 145 150 155 160
 Pro Gly Ala Asp Ala Leu Leu Gln Pro Gln Trp Pro Leu Leu Val Asn
 165 170 175
 Gly Cys Pro Tyr Thr Gly Asp Asn Tyr Gln Thr Lys Leu Ile Pro Val
 180 185 190
 Trp Glu Ala Ser Asp Leu Pro Phe Pro Ser His Tyr Gln Arg Phe Ser
 195 200 205
 Ile Ser Thr Phe Ser Phe Val Asp Ser Val Ala Lys Arg Ala Leu Lys
 210 215 220
 Gly Pro Val Tyr Leu His Cys Ser Ala Ser Val Cys Gln Pro Ala Gly
 225 230 235 240
 Thr Pro Ser Cys Val Thr Leu Cys Pro Ala Arg Arg Arg Arg Ser Ser
 245 250 255
 Asp Ile His Phe Gln Asn Lys Thr Ala Ser Ile Ser Ser Lys Gly Pro
 260 265 270
 Leu Ile Leu Leu Gln Ala Ile Gln Asp Ser Ser Glu Lys Leu His Lys
 275 280 285
 Tyr Ser Arg Ser Pro Val Asp Ser Gln Ala Leu Trp Val Ala Gly Leu
 290 295 300
 Ser Gly Ile Leu Ile Val Gly Ala Leu Phe Met Ser Tyr Leu Ala Ile
 305 310 315 320
 Arg Lys Trp Arg

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bos taurus
- (D) DEVELOPMENTAL STAGE: Juvenile
- (E) HAPLOTYPE: Diploidy
- (F) TISSUE TYPE: Ovary
- (G) CELL TYPE: Oocyte

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 149..1411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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CCCGGGCCCTC CCTACTCTCA GGAAGGCACC CGCTCACCTC CTCAGTTCT CGATCTCGGC      60
CGGGATGCTC TGAAGCTGGT TGCCGCCGAG GCTGAGGGTC TGCAGCGGCG CAGTCCAGCA      120
GCCAGGTGGG AGTGGCTTCG TGGGCACC ATG GGG CCG TGC TCT AGG CTG TTC      172
                               Met Gly Pro Cys Ser Arg Leu Phe
                               1                               5

GTC TGC TTT CTG CTC TGG GGA AGC ACA GAG CTC TGC AGC CCC CAG CCC      220
Val Cys Phe Leu Leu Trp Gly Ser Thr Glu Leu Cys Ser Pro Gln Pro
   10                               15                               20

TTC TGG GAT GAT GAA ACC GAG CGC TTC AGG CCA TCA AAG CCG CCC GCC      268
Phe Trp Asp Asp Glu Thr Glu Arg Phe Arg Pro Ser Lys Pro Pro Ala
   25                               30                               35                               40

GTG ATG GTG GAG TGT CAG GAG GCC CAG CTG GTG GTC ACA GTC GAC AAA      316
Val Met Val Glu Cys Gln Glu Ala Gln Leu Val Val Thr Val Asp Lys
                               45                               50                               55

GAC CTT TTC GGC ACA GGG AAG CTC ATC CGG CCT GCG GAC CTC ACC CTG      364
Asp Leu Phe Gly Thr Gly Lys Leu Ile Arg Pro Ala Asp Leu Thr Leu
                               60                               65                               70

GGC CCC GAC AAC TGT GAG CCG CTG GCC TCC GCG GAC ACG GAT GGC GTG      412
Gly Pro Asp Asn Cys Glu Pro Leu Ala Ser Ala Asp Thr Asp Gly Val
                               75                               80                               85

GTT AGG TTT GCG GTC GGG CTG CAC GAG TGT GGC AAC ATC TTG CAG GTG      460
Val Arg Phe Ala Val Gly Leu His Glu Cys Gly Asn Ile Leu Gln Val
   90                               95                               100

ACC GAC AAT GCC CTG GTG TAC AGC ACC TTC CTG CTC CAC AAC CCC CGC      508
Thr Asp Asn Ala Leu Val Tyr Ser Thr Phe Leu Leu His Asn Pro Arg
  105                               110                               115                               120

CCT GCA GGA AAC CTG TCC ATC CTG AGG ACT AAC CGC GCA GAG GTC CCC      556
Pro Ala Gly Asn Leu Ser Ile Leu Arg Thr Asn Arg Ala Glu Val Pro
                               125                               130                               135

ATC GAG TGC CAC TAC CCC AGG CAG GGC AAT GTG AGT AGC TGG GCC ATC      604
Ile Glu Cys His Tyr Pro Arg Gln Gly Asn Val Ser Ser Trp Ala Ile
                               140                               145                               150

CAG CCC ACC TGG GTG CCA TTC AGG ACC ACA GTG TTC TCG GAG GAG AAG      652
Gln Pro Thr Trp Val Pro Phe Arg Thr Thr Val Phe Ser Glu Glu Lys
                               155                               160                               165

CTG GTT TTC TCT CTG CGC CTG ATG GAG GAG AAC TGG AGC GCC GAG AAG      700
Leu Val Phe Ser Leu Arg Leu Met Glu Glu Asn Trp Ser Ala Glu Lys
  170                               175                               180

ATG ACG CCC ACC TTC CAG CTG GGA GAC AGA GCC CAC CTC CAG GCC CAA      748
Met Thr Pro Thr Phe Gln Leu Gly Asp Arg Ala His Leu Gln Ala Gln
  185                               190                               195                               200

GTG CAC ACT GGC AGC CAC GTG CCC CTG CGG CTG TTC GTG GAC CAC TGC      796
Val His Thr Gly Ser His Val Pro Leu Arg Leu Phe Val Asp His Cys
                               205                               210                               215

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GTG GCC AGC CTG ACG CCA GAC TGG AGC ACC TCC CCT TAC CAC ACC ATC Val Ala Ser Leu Thr Pro Asp Trp Ser Thr Ser Pro Tyr His Thr Ile 220 225 230	844
GTG GAC TTC CAT GGT TGT CTC GTC GAT GGT CTC ACC GAT GCC TCC TCT Val Asp Phe His Gly Cys Leu Val Asp Gly Leu Thr Asp Ala Ser Ser 235 240 245	892
GCT TTC AAA GCA CCC AGA CCC AGA CCG GAG ATC CTC CAG TTC ACA GTG Ala Phe Lys Ala Pro Arg Pro Arg Pro Glu Ile Leu Gln Phe Thr Val 250 255 260	940
GAT GTG TTC CGT TTT GCT AAT GAC TCC AGA AAC ATG ATA TAT ATC ACC Asp Val Phe Arg Phe Ala Asn Asp Ser Arg Asn Met Ile Tyr Ile Thr 265 270 275 280	988
TGC CAC CTG AAG GTC ACT CCG GTT GAC CGA GTC CCG GAC CAA CTA AAC Cys His Leu Lys Val Thr Pro Val Asp Arg Val Pro Asp Gln Leu Asn 285 290 295	1036
AAA GCC TGT TCC TTC AGC AAG TCC TCC AAC AGG TGG TCC CCG GTT GAA Lys Ala Cys Ser Phe Ser Lys Ser Ser Asn Arg Trp Ser Pro Val Glu 300 305 310	1084
GGC CCC ACT GAC ATC TGT CGA TGC TGT AGC AAG GGG CGC TGT GGC ATT Gly Pro Thr Asp Ile Cys Arg Cys Cys Ser Lys Gly Arg Cys Gly Ile 315 320 325	1132
TCA GGC CGT TCC ATG AGG CTG TCC CAC CGG GAG GGC AGG CCT GTT CCC Ser Gly Arg Ser Met Arg Leu Ser His Arg Glu Gly Arg Pro Val Pro 330 335 340	1180
CGA AGT CGC AGG CAC GTG ACG GAG GAA GCA GAT GTC ACC GTG GGG CCG Arg Ser Arg Arg His Val Thr Glu Glu Ala Asp Val Thr Val Gly Pro 345 350 355 360	1228
TTG ATC TTC CTG AGG AAG ATG AAT GAC CGT GGC GTG GAA GGG CCC ACC Leu Ile Phe Leu Arg Lys Met Asn Asp Arg Gly Val Glu Gly Pro Thr 365 370 375	1276
TCC TCT CCC CCT CTG GTG ATG CTG GGC TTA GGC CTG GCT ACT GTG ATG Ser Ser Pro Pro Leu Val Met Leu Gly Leu Gly Leu Ala Thr Val Met 380 385 390	1324
ACC TTG ACT CTG GCT GCC ATT GTC CTG GGT CTC ACT GGG AGG CTT CCG Thr Leu Thr Leu Ala Ala Ile Val Leu Gly Leu Thr Gly Arg Leu Arg 395 400 405	1372
GCT GCT TCT CAC CCC GTG TGC CCT GTG TCT GCT TCC CAA TAAAAGAAGA Ala Ala Ser His Pro Val Cys Pro Val Ser Ala Ser Gln 410 415 420	1421
AAGTGAAAAA AAAAAAAAAA AAGCGGCCGC GAATTC	1457

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Pro Cys Ser Arg Leu Phe Val Cys Phe Leu Leu Trp Gly Ser

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1	5	10	15
Thr Glu Leu Cys Ser Pro Gln Pro Phe Trp Asp Asp Glu Thr Glu Arg	20	25	30
Phe Arg Pro Ser Lys Pro Pro Ala Val Met Val Glu Cys Gln Glu Ala	35	40	45
Gln Leu Val Val Thr Val Asp Lys Asp Leu Phe Gly Thr Gly Lys Leu	50	55	60
Ile Arg Pro Ala Asp Leu Thr Leu Gly Pro Asp Asn Cys Glu Pro Leu	65	70	75
Ala Ser Ala Asp Thr Asp Gly Val Val Arg Phe Ala Val Gly Leu His	85	90	95
Glu Cys Gly Asn Ile Leu Gln Val Thr Asp Asn Ala Leu Val Tyr Ser	100	105	110
Thr Phe Leu Leu His Asn Pro Arg Pro Ala Gly Asn Leu Ser Ile Leu	115	120	125
Arg Thr Asn Arg Ala Glu Val Pro Ile Glu Cys His Tyr Pro Arg Gln	130	135	140
Gly Asn Val Ser Ser Trp Ala Ile Gln Pro Thr Trp Val Pro Phe Arg	145	150	155
Thr Thr Val Phe Ser Glu Glu Lys Leu Val Phe Ser Leu Arg Leu Met	165	170	175
Glu Glu Asn Trp Ser Ala Glu Lys Met Thr Pro Thr Phe Gln Leu Gly	180	185	190
Asp Arg Ala His Leu Gln Ala Gln Val His Thr Gly Ser His Val Pro	195	200	205
Leu Arg Leu Phe Val Asp His Cys Val Ala Ser Leu Thr Pro Asp Trp	210	215	220
Ser Thr Ser Pro Tyr His Thr Ile Val Asp Phe His Gly Cys Leu Val	225	230	235
Asp Gly Leu Thr Asp Ala Ser Ser Ala Phe Lys Ala Pro Arg Pro Arg	245	250	255
Pro Glu Ile Leu Gln Phe Thr Val Asp Val Phe Arg Phe Ala Asn Asp	260	265	270
Ser Arg Asn Met Ile Tyr Ile Thr Cys His Leu Lys Val Thr Pro Val	275	280	285
Asp Arg Val Pro Asp Gln Leu Asn Lys Ala Cys Ser Phe Ser Lys Ser	290	295	300
Ser Asn Arg Trp Ser Pro Val Glu Gly Pro Thr Asp Ile Cys Arg Cys	305	310	315
Cys Ser Lys Gly Arg Cys Gly Ile Ser Gly Arg Ser Met Arg Leu Ser	325	330	335
His Arg Glu Gly Arg Pro Val Pro Arg Ser Arg Arg His Val Thr Glu	340	345	350
Glu Ala Asp Val Thr Val Gly Pro Leu Ile Phe Leu Arg Lys Met Asn	355	360	365

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Asp Arg Gly Val Glu Gly Pro Thr Ser Ser Pro Pro Leu Val Met Leu
 370 375 380

Gly Leu Gly Leu Ala Thr⁴ Val Met Thr Leu Thr Leu Ala Ala Ile Val
 385 390 395 400

Leu Gly Leu Thr Gly Arg Leu Arg Ala Ala Ser His Pro Val Cys Pro
 405 410 415

Val Ser Ala Ser Gln
 420

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTTCGTGCT TATCTGAACA TGTCTTGAGG GATTAGTATG TGTGCTCATT TGGGTTCTTT 60
 CCGCTGTATG CTAGGCGTAT CTAGATGCAT TAGCTTGTTA ACACCTCATG TGGAGTAAAA 120
 GATGT 125

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGGCGTAGG CGTGGACTGA AGTTCAAAGC CATGCCCCG TTCTGATAGC ATACGTTTGA 60
 AATGTCATTG TAGTTGCATG GCTGTATAAG CCAGTCTCAT AGATAAGGGA A 111

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCGGTCGGTC ATGTGATGCT GCGTATAGTA CGATTGTA TGCATTATGC GAAATTATTC 60
 TAACGACCCG CGATATGGAG GTTGGATTAA GTTACA 96

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(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGGARAGRT GYCAMGARG

19

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCTAAGGA AGATCTATGG ATCC

24

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCTAAGGA GGTGTATGG ATCC

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCTATGAC CATGATTACG GATTGCGTA GCCGTCGTCC TGCAGCGTCG CGACT

55

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGAAAACCC GGGCGTTACC CAACTTAATC GATTAGCAGC ACATCCCCCT TCGCCAG 57

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTCCCACT CGCGCTGCAG AACGACGGCT AGCGAATCCG TAATCATGGT CATA 54

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTGGCCAAAG GGGGATGTGG CTGCTAATCG ATTAAGTTGG GTAACGCCCCG GG 52

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCTATGAC CATGATTACG GATTCGCTAG CCGTCGTTCT GCAGCGTCGC GACTGGGAAA 60

ATACTGGTAC TAATGCCTAA GCGATCGGCA GCAAGACGTC GGAGCGCTGAC CCTTTACCC 120

GGGCGTTACC CAACTTAATC GATTAGCAGC ACATCCCCCT TTCGCCAGTGG GCCCGCAAT 180

CCCTTGAATT AGCAAATCGT CGTGTAGGGG GAAAGCGGTC 120

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(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCCAAGCTTC CGACACCATC GAACGGCGC

29

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGCACAATG TGCCTAATGA GTGAGCTAAC

30

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCGGATCCG GACGAAGGCC AGCGCTTG

28

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCGGTCGACT CATTATGAT GATGATGATG ATGCGGGCTC GAGGTGGACC CTTCCACC

58

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:

- 119 -

- (A) LENGTH: 1701 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATG TGG CTG CTG CGG TGC GTT TTG CTG TGT GTT TCA TTA TCT CTT GCT	48
Met Trp Leu Leu Arg Cys Val Leu Leu Cys Val Ser Leu Ser Leu Ala	
1 5 10 15	
GTG AGT GGC CAG CAT AAG CCT GAG GCA CCA GAT TAT TCC AGT GTG CTC	96
Val Ser Gly Gln His Lys Pro Glu Ala Pro Asp Tyr Ser Ser Val Leu	
20 25 30	
CAC TGT GGG CCG TGG AGC TTC CAG TTT GCT GTA AAC CTC AAC CAG GAG	144
His Cys Gly Pro Trp Ser Phe Gln Phe Ala Val Asn Leu Asn Gln Glu	
35 40 45	
GCA ACG TCT CCT CCT GTA CTA ATA GCT TGG GAC AAC CAA GGG CTG CTG	192
Ala Thr Ser Pro Pro Val Leu Ile Ala Trp Asp Asn Gln Gly Leu Leu	
50 55 60	
CAC GAG CTG CAG AAT GAC TCC GAC TGT GGC ACC TGG ATA AGA AAA GGT	240
His Glu Leu Gln Asn Asp Ser Asp Cys Gly Thr Trp Ile Arg Lys Gly	
65 70 75 80	
CCA GGC AGC TCC GTG GTG TTG GAG GCA ACC TAT AGC AGC TGC TAT GTC	288
Pro Gly Ser Ser Val Val Leu Glu Ala Thr Tyr Ser Ser Cys Tyr Val	
85 90 95	
ACT GAG TGG GTG AGT ATG ACC CAA TGG CCA GGG AGA CTG TGT GAA GCG	336
Thr Glu Trp Val Ser Met Thr Gln Trp Pro Gly Arg Leu Cys Glu Ala	
100 105 110	
CCT CAT GCT ACC ATC CAG GCT GAC CCC CAA GGC CTG TCT CTC CAG GAC	384
Pro His Ala Thr Ile Gln Ala Asp Pro Gln Gly Leu Ser Leu Gln Asp	
115 120 125	
TCC CAC TAC ATC ATG CCA GTT GGA GTT GAA GGA GCA GGC GCG GCT GAA	432
Ser His Tyr Ile Met Pro Val Gly Val Glu Gly Ala Gly Ala Ala Glu	
130 135 140	
CAC AAG GTG GTT ACA GAG AGG AAG CTG CTC AAG TGT CCT ATG GAT CTT	480
His Lys Val Val Thr Glu Arg Lys Leu Leu Lys Cys Pro Met Asp Leu	
145 150 155 160	
CTA GAT GCT CCA GAT ACT GAC TGG TGT GAC TCC ATC CCA GCA CGG GAC	528
Leu Asp Ala Pro Asp Thr Asp Trp Cys Asp Ser Ile Pro Ala Arg Asp	
165 170 175	
AGA CTG CCA TGT GCA CCT TCA CCC ATC TCT CGA GGA GAC TGT GAA GGG	576
Arg Leu Pro Cys Ala Pro Ser Pro Ile Ser Arg Gly Asp Cys Glu Gly	
180 185 190	
CTA GGC TGT TGT TAT AGC TCT GAA GAG GTG AAT TCC TGC TAC TAT GGA	624
Leu Gly Cys Cys Tyr Ser Ser Glu Val Asn Ser Cys Tyr Tyr Gly	
195 200 205	

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AAC Asn	ACT Thr	GTG Val	ACC Thr	TTG Leu	CAT His	TGT Cys	ACC Thr	CGA Arg	GAG Glu	GGC Gly	CAT His	TTC Phe	TCT Ser	ATT Ile	GCT Ala	672
210						215					220					
GTG Val	TCT Ser	CGG Arg	AAC Asn	GTG Val	ACC Thr	TCG Ser	CCA Pro	CCA Pro	CTG Leu	CTC Leu	TTG Leu	GAT Asp	TCT Ser	GTG Val	CGC Arg	720
225						230				235					240	
TTG Leu	GCC Ala	CTT Leu	AGG Arg	AAT Asn	GAC Asp	AGT Ser	GCG Ala	TGT Cys	AAC Asn	CCT Pro	GTG Val	ATG Met	GCA Ala	ACA Thr	CAA Gln	768
				245					250					255		
GCT Ala	TTT Phe	GTT Val	CTG Leu	TTC Phe	CAG Gln	TTT Phe	CCA Pro	TTT Phe	ACT Thr	TCC Ser	TGT Cys	GGC Gly	ACC Thr	ACA Thr	AGA Arg	816
			260					265					270			
CAG Gln	ATC Ile	ACT Thr	GGA Gly	GAC Asp	CGA Arg	GCA Ala	GTA Val	TAT Tyr	GAA Glu	AAT Asn	GAA Glu	CTG Leu	GTG Val	GCA Ala	ACT Thr	864
		275					280					285				
AGG Arg	GAT Asp	GTG Val	AAA Lys	AAT Asn	GGG Gly	AGC Ser	CGT Arg	GGC Gly	TCT Ser	GTC Val	ACT Thr	CGT Arg	GAC Asp	AGC Ser	ATC Ile	912
	290					295					300					
TTC Phe	AGG Arg	CTC Leu	CAT His	GTC Val	AGC Ser	TGC Cys	AGC Ser	TAC Tyr	TCA Ser	GTA Val	AGT Ser	AGC Ser	AAC Asn	TCT Ser	CTC Leu	960
305					310					315					320	
CCA Pro	ATC Ile	AAT Asn	GTC Val	CAG Gln	GTT Val	TTC Phe	ACT Thr	CTC Leu	CCA Pro	CCA Pro	CCC Pro	TTT Phe	CCT Pro	GAG Glu	ACC Thr	1008
				325					330					335		
CAG Gln	CCT Pro	GGA Gly	CCC Pro	CTC Leu	ACT Thr	CTG Leu	GAA Glu	CTT Leu	CAG Gln	ATT Ile	GCC Ala	AAA Lys	GAT Asp	AAA Lys	AAC Asn	1056
			340					345					350			
TAT Tyr	GGC Gly	TCT Ser	TAC Tyr	TAC Tyr	GGT Gly	GTT Val	GGT Gly	GAC Asp	TAC Tyr	CCA Pro	GTG Val	GTG Val	AAG Lys	TGT Leu	CTT Leu	1104
	355					360						365				
CGG Arg	GAT Asp	CCC Pro	ATT Ile	TAC Tyr	GTG Val	GAG Glu	GTC Val	TCC Ser	ATC Ile	CTT Leu	CAC His	AGA Arg	ACA Thr	GAC Asp	CCC Pro	1152
	370					375					380					
TAC Tyr	CTG Leu	GGG Gly	CTG Leu	CTC Leu	CTA Leu	CAA Gln	CAG Gln	TGT Cys	TGG Trp	GCA Ala	ACA Thr	CCC Pro	AGC Ser	ACT Thr	GAC Asp	1200
	385				390					395					400	
CCC Pro	CTG Leu	AGT Ser	CAG Gln	CCA Pro	CAG Gln	TGG Trp	CCC Pro	ATC Ile	CTG Leu	GTA Val	AAG Lys	GGC Gly	TGC Cys	CCC Pro	TAC Tyr	1248
				405					410					415		
ATT Ile	GGA Gly	GAC Asp	AAC Asn	TAT Tyr	CAG Gln	ACC Thr	CAG Gln	CTG Leu	ATC Ile	CCT Pro	GTC Val	CAG Gln	AAA Lys	GCC Ala	TTG Leu	1296
			420					425					430			
GAT Asp	CTT Leu	CCA Pro	TTT Phe	CCC Pro	TCT Ser	CAC His	CAC His	CAG Gln	CGC Arg	TTC Phe	AGC Ser	ATC Ile	TTC Phe	ACC Thr	TTC Phe	1344
		435					440					445				
AGC Ser	TTT Phe	GTG Val	AAC Asn	CCT Pro	ACA Thr	GTG Val	GAG Glu	AAA Lys	CAG Gln	GCC Ala	CTC Leu	AGG Arg	GGA Gly	CCG Pro	GTG Val	1392
	450					455					460					
CAT His	CTG Leu	CAC His	TGC Cys	AGC Ser	GTG Val	TCA Ser	GTC Val	TGC Cys	CAG Gln	CCT Pro	GCT Ala	GAG Glu	ACA Thr	CCA Pro	TCC Ser	1440
465					470					475					480	

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TGT GTG GTG ACC TGT CCT GAT CTC AGT CGA AGA AGA AAT TTT GAC AAC	1488
Cys Val Val Thr Cys Pro Asp Leu Ser Arg Arg Arg Asn Phe Asp Asn	
485 490 495	
AGT TCT CAG AAC ACT ACT GCT AGT GTT TCT AGC AAA GGC CCC ATG ATT	1536
Ser Ser Gln Asn Thr Thr Ala Ser Val Ser Ser Lys Gly Pro Met Ile	
500 505 510	
CTA CTC CAA GCC ACT AAG GAC CCT CCA GAA AAG CTC CGT GTT CCT GTA	1584
Leu Leu Gln Ala Thr Lys Asp Pro Pro Glu Lys Leu Arg Val Pro Val	
515 520 525	
GAC TCG AAA GTT CTG TGG GTG GCA GGC CTT TCT GGG ACC TTA ATC CTT	1632
Asp Ser Lys Val Leu Trp Val Ala Gly Leu Ser Gly Thr Leu Ile Leu	
530 535 540	
GGA GCC TTG TTA GTA TCC TAC TTG GCT GTC AAG AAA CAG AAG AGT TGC	1680
Gly Ala Leu Leu Val Ser Tyr Leu Ala Val Lys Lys Gln Lys Ser Cys	
545 550 555 560	
CCA GAC CAA ATG TGT CAA TAA	1701
Pro Asp Gln Met Cys Gln	
565	

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Trp	Leu	Leu	Arg	Cys	Val	Leu	Leu	Cys	Val	Ser	Leu	Ser	Leu	Ala
1				5					10						15
Val	Ser	Gly	Gln	His	Lys	Pro	Glu	Ala	Pro	Asp	Tyr	Ser	Ser	Val	Leu
			20					25					30		
His	Cys	Gly	Pro	Trp	Ser	Phe	Gln	Phe	Ala	Val	Asn	Leu	Asn	Gln	Glu
		35					40					45			
Ala	Thr	Ser	Pro	Pro	Val	Leu	Ile	Ala	Trp	Asp	Asn	Gln	Gly	Leu	Leu
		50				55					60				
His	Glu	Leu	Gln	Asn	Asp	Ser	Asp	Cys	Gly	Thr	Trp	Ile	Arg	Lys	Gly
		65			70					75					80
Pro	Gly	Ser	Ser	Val	Val	Leu	Glu	Ala	Thr	Tyr	Ser	Ser	Cys	Tyr	Val
				85					90					95	
Thr	Glu	Trp	Val	Ser	Met	Thr	Gln	Trp	Pro	Gly	Arg	Leu	Cys	Glu	Ala
			100					105					110		
Pro	His	Ala	Thr	Ile	Gln	Ala	Asp	Pro	Gln	Gly	Leu	Ser	Leu	Gln	Asp
			115				120					125			
Ser	His	Tyr	Ile	Met	Pro	Val	Gly	Val	Glu	Gly	Ala	Gly	Ala	Ala	Glu
			130			135					140				
His	Lys	Val	Val	Thr	Glu	Arg	Lys	Leu	Leu	Lys	Cys	Pro	Met	Asp	Leu
					150					155					160
Leu	Asp	Ala	Pro	Asp	Thr	Asp	Trp	Cys	Asp	Ser	Ile	Pro	Ala	Arg	Asp

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165										170					175						
Arg	Leu	Pro	Cys 180	Ala	Pro 185	Ser	Pro	Ile	Ser	Arg	Gly	Asp	Cys 190	Glu	Gly						
Leu	Gly	Cys 195	Cys	Tyr	Ser	Ser	Glu	Glu	Val	Asn	Ser	Cys 205	Tyr	Tyr	Gly						
Asn	Thr 210	Val	Thr	Leu	His	Cys 215	Thr	Arg	Glu	Gly	His 220	Phe	Ser	Ile	Ala						
Val 225	Ser	Arg	Asn	Val	Thr 230	Ser	Pro	Pro	Leu	Leu 235	Leu	Asp	Ser	Val	Arg 240						
Leu	Ala	Leu	Arg	Asn 245	Asp	Ser	Ala	Cys	Asn 250	Pro	Val	Met	Ala	Thr 255	Gln						
Ala	Phe	Val	Leu 260	Phe	Gln	Phe	Pro	Phe 265	Thr	Ser	Cys	Gly	Thr 270	Thr	Arg						
Gln	Ile	Thr 275	Gly	Asp	Arg	Ala	Val 280	Tyr	Glu	Asn	Glu	Leu 285	Val	Ala	Thr						
Arg	Asp 290	Val	Lys	Asn	Gly	Ser 295	Arg	Gly	Ser	Val	Thr 300	Arg	Asp	Ser	Ile						
Phe 305	Arg	Leu	His	Val	Ser 310	Cys	Ser	Tyr	Ser	Val 315	Ser	Ser	Asn	Ser	Leu 320						
Pro	Ile	Asn	Val	Gln 325	Val	Phe	Thr	Leu	Pro 330	Pro	Pro	Phe	Pro	Glu 335	Thr						
Gln	Pro	Gly	Pro 340	Leu	Thr	Leu	Glu	Leu 345	Gln	Ile	Ala	Lys	Asp 350	Lys	Asn						
Tyr	Gly	Ser 355	Tyr	Tyr	Gly	Val	Gly 360	Asp	Tyr	Pro	Val	Val 365	Lys	Leu	Leu						
Arg	Asp 370	Pro	Ile	Tyr	Val	Glu 375	Val	Ser	Ile	Leu	His 380	Arg	Thr	Asp	Pro						
Tyr 385	Leu	Gly	Leu	Leu	Leu 390	Gln	Gln	Cys	Trp	Ala 395	Thr	Pro	Ser	Thr	Asp 400						
Pro	Leu	Ser	Gln	Pro 405	Gln	Trp	Pro	Ile	Leu 410	Val	Lys	Gly	Cys	Pro 415	Tyr						
Ile	Gly	Asp	Asn 420	Tyr	Gln	Thr	Gln	Leu 425	Ile	Pro	Val	Gln	Lys	Ala	Leu						
Asp	Leu	Pro 435	Phe	Pro	Ser	His	His 440	Gln	Arg	Phe	Ser	Ile 445	Phe	Thr	Phe						
Ser	Phe 450	Val	Asn	Pro	Thr	Val 455	Glu	Lys	Gln	Ala	Leu 460	Arg	Gly	Pro	Val						
His 465	Leu	His	Cys	Ser	Val 470	Ser	Val	Cys	Gln	Pro 475	Ala	Glu	Thr	Pro	Ser 480						
Cys	Val	Val	Thr	Cys 485	Pro	Asp	Leu	Ser	Arg 490	Arg	Arg	Asn	Phe	Asp 495	Asn						
Ser	Ser	Gln	Asn 500	Thr	Thr	Ala	Ser	Val 505	Ser	Ser	Lys	Gly	Pro 510	Met	Ile						
Leu	Leu	Gln 515	Ala	Thr	Lys	Asp	Pro 520	Pro	Glu	Lys	Leu	Arg 525	Val	Pro	Val						

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Asp Ser Lys Val Leu Trp Val Ala Gly Leu Ser Gly Thr Leu Ile Leu
 530 535 540

Gly Ala Leu Leu Val Ser Tyr Leu Ala Val Lys Lys Gln Lys Ser Cys
 545 550 555 560

Pro Asp Gln Met Cys Gln
 565

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG GCG TGC AGG CAG AGA GGA GGC TCT TGG AGT CCC TCA GGC TGG TTC	48
Met Ala Cys Arg Gln Arg Gly Gly Ser Trp Ser Pro Ser Gly Trp Phe	
1 5 10 15	
AAT GCA GGC TGG AGC ACC TAC AGG TCG ATT TCT CTC TTC TTC GCC CTT	96
Asn Ala Gly Trp Ser Thr Tyr Arg Ser Ile Ser Leu Phe Phe Ala Leu	
20 25 30	
GTG ACT TCA GGG AAC TCC ATA GAT GTT TCT CAG TTG GTA AAT CCT GCC	144
Val Thr Ser Gly Asn Ser Ile Asp Val Ser Gln Leu Val Asn Pro Ala	
35 40 45	
TTT CCA GGC ACT GTC ACT TGC GAT GAA AGG GAA ATA ACA GTG GAG TTC	192
Phe Pro Gly Thr Val Thr Cys Asp Glu Arg Glu Ile Thr Val Glu Phe	
50 55 60	
CCA AGC AGT CCT GGC ACC AAG AAA TGG CAT GCA TCT GTG GTG GAT CCT	240
Pro Ser Ser Pro Gly Thr Lys Lys Trp His Ala Ser Val Val Asp Pro	
65 70 75 80	
CTT GGT CTC GAC ATG CCG AAC TGC ACT TAC ATC CTG GAC CCA GAA AAG	288
Leu Gly Leu Asp Met Pro Asn Cys Thr Tyr Ile Leu Asp Pro Glu Lys	
85 90 95	
CTC ACC CTG AGG GCT ACC TAT GAT AAC TGT ACC AGG AGA GTG CAT GGT	336
Leu Thr Leu Arg Ala Thr Tyr Asp Asn Cys Thr Arg Arg Val His Gly	
100 105 110	
GGA CAC CAG ATG ACC ATC AGA GTC ATG AAC AAC AGT GCT GCC TTA AGA	384
Gly His Gln Met Thr Ile Arg Val Met Asn Asn Ser Ala Ala Leu Arg	
115 120 125	
CAC GGA GCT GTC ATG TAT CAG TTC TTC TGT CCA GCT ATG CAA GTA GAA	432
His Gly Ala Val Met Tyr Gln Phe Phe Cys Pro Ala Met Gln Val Glu	
130 135 140	
GAG ACC CAG GGG CTT TCA GCA TCT ACA ATC TGC CAG AAG GAT TTC ATG	480
Glu Thr Gln Gly Leu Ser Ala Ser Thr Ile Cys Gln Lys Asp Phe Met	
145 150 155 160	

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TCT TTT TCC TTG CCA CGG GTC TTC TCT GGC TTG GCT GAC GAC AGT AAG Ser Phe Ser Leu Pro Arg Val Phe Ser Gly Leu Ala Asp Asp Ser Lys 165 170 175	528
GGG ACC AAA GTT CAG ATG GGA TGG AGC ATT GAG GTT GGT GAT GGT GCA Gly Thr Lys Val Gln Met Gly Trp Ser Ile Glu Val Gly Asp Gly Ala 180 185 190	576
AGA GCC AAA ACT CTG ACC CTG CCA GAG GCC ATG AAG GAA GGC TTC AGC Arg Ala Lys Thr Leu Thr Leu Pro Glu Ala Met Lys Glu Gly Phe Ser 195 200 205	624
CTC TTG ATT GAC AAC CAC AGG ATG ACC TTC CAT GTG CCA TTC AAT GCC Leu Leu Ile Asp Asn His Arg Met Thr Phe His Val Pro Phe Asn Ala 210 215 220	672
ACT GGA GTG ACT CAC TAT GTG CAA GGT AAC AGT CAT CTC TAC ATG GTG Thr Gly Val Thr His Tyr Val Gln Gly Asn Ser His Leu Tyr Met Val 225 230 235 240	720
TCT CTG AAG CTT ACA TTT ATA TCT CCT GGA CAG AAG GTG ATC TTC TCT Ser Leu Lys Leu Thr Phe Ile Ser Pro Gly Gln Lys Val Ile Phe Ser 245 250 255	768
TCA CAA GCT ATT TGT GCA CCA GAT CCT GTG ACC TGC AAT GCC ACA CAC Ser Gln Ala Ile Cys Ala Pro Asp Pro Val Thr Cys Asn Ala Thr His 260 265 270	816
ATG ACT CTC ACC ATA CCA GAG TTT CCT GGG AAG CTT AAG TCT GTG AGC Met Thr Leu Thr Ile Pro Glu Phe Pro Gly Lys Leu Lys Ser Val Ser 275 280 285	864
TTT GAA AAC CAG AAC ATT GAT GTG AGC CAG CTG CAT GAC AAT GGA ATT Phe Glu Asn Gln Asn Ile Asp Val Ser Gln Leu His Asp Asn Gly Ile 290 295 300	912
GAT CTA GAA GCA ACA AAT GGC ATG AAA TTG CAT TTC AGC AAA ACT CTG Asp Leu Glu Ala Thr Asn Gly Met Lys Leu His Phe Ser Lys Thr Leu 305 310 315 320	960
CTC AAA ACG AAA TTA TCT GAA AAA TGC CTA CTC CAT CAG TTC TAC TTA Leu Lys Thr Lys Leu Ser Glu Lys Cys Leu Leu His Gln Phe Tyr Leu 325 330 335	1008
GCT TCA CTC AAG CTG ACC TTT CTC CTT CGG CCA GAG ACA GTA TCC ATG Ala Ser Leu Lys Leu Thr Phe Leu Leu Arg Pro Glu Thr Val Ser Met 340 345 350	1056
GTG ATC TAT CCT GAG TGT CTC TGT GAG TCA CCC GTT TCT ATA GTT ACA Val Ile Tyr Pro Glu Cys Leu Cys Glu Ser Pro Val Ser Ile Val Thr 355 360 365	1104
GGG GAG CTG TGC ACC CAG GAT GGG TTT ATG GAC GTC GAG GTC TAC AGC Gly Glu Leu Cys Thr Gln Asp Gly Phe Met Asp Val Glu Val Tyr Ser 370 375 380	1152
TAC CAA ACA CAA CCA GCT CTT GAC CTG GGT ACT CTG AGG GTG GGA AAC Tyr Gln Thr Gln Pro Ala Leu Asp Leu Gly Thr Leu Arg Val Gly Asn 385 390 395 400	1200
TCA TCC TGC CAG CCT GTC TTT GAG GCT CAG TCT CAG GGG CTG GTA CGG Ser Ser Cys Gln Pro Val Phe Glu Ala Gln Ser Gln Gly Leu Val Arg 405 410 415	1248
TTC CAC ATA CCC CTG AAT GGA TGT GGA ACG AGA TAT AAG TTC GAA GAT Phe His Ile Pro Leu Asn Gly Cys Gly Thr Arg Tyr Lys Phe Glu Asp 420 425 430	1296

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GAT AAA GTC GTC TAT GAA AAC GAA ATA CAT GCT CTC TGG ACG GAT TTT Asp Lys Val Val Tyr Glu Asn Glu Ile His Ala Leu Trp Thr Asp Phe 435 440 445	1344
CCT CCA AGC AAA ATA TCT AGA GAC AGT GAG TTC AGA ATG ACA GTG AAG Pro Pro Ser Lys Ile Ser Arg Asp Ser Glu Phe Arg Met Thr Val Lys 450 455 460	1392
TGT TCT TAT AGC AGG AAT GAC ATG CTA CTA AAC ATC AAC GTT GAA AGC Cys Ser Tyr Ser Arg Asn Asp Met Leu Leu Asn Ile Asn Val Glu Ser 465 470 475 480	1440
CTT ACT CCT CCA GTG GCC TCA GTG AAG TTG GGT CCA TTT ACC TTG ATC Leu Thr Pro Pro Val Ala Ser Val Lys Leu Gly Pro Phe Thr Leu Ile 485 490 495	1488
CTG CAA AGC TAC CCA GAT AAT TCC TAC CAA CAA CCT TAT GGG GAA AAC Leu Gln Ser Tyr Pro Asp Asn Ser Tyr Gln Gln Pro Tyr Gly Glu Asn 500 505 510	1536
GAG TAC CCT CTA GTG AGA TTC CTC CGC CAA CCA ATT TAC ATG GAA GTG Glu Tyr Pro Leu Val Arg Phe Leu Arg Gln Pro Ile Tyr Met Glu Val 515 520 525	1584
AGA GTC CTA AAC AGG GAT GAC CCC AAC ATC AAG CTG GTC TTA GAT GAC Arg Val Leu Asn Arg Asp Asp Pro Asn Ile Lys Leu Val Leu Asp Asp 530 535 540	1632
TGC TGG GCG ACG TCC ACC ATG GAT CCA GAC TCT TTC CCC CAG TGG AAC Cys Trp Ala Thr Ser Thr Met Asp Pro Asp Ser Phe Pro Gln Trp Asn 545 550 555 560	1680
GTT GTC GTG GAT GGC TGT GCA TAT GAC CTG GAC AAC TAC CAG ACC ACC Val Val Val Asp Gly Cys Ala Tyr Asp Leu Asp Asn Tyr Gln Thr Thr 565 570 575	1728
TTC CAT CCA GTC GGC TCC TCT GTG ACC CAT CCT GAT CAC TAT CAG AGG Phe His Pro Val Gly Ser Ser Val Thr His Pro Asp His Tyr Gln Arg 580 585 590	1776
TTT GAC ATG AAG GCT TTT GCC TTT GTA TCA GAA GCC CAC GTG CTC TCT Phe Asp Met Lys Ala Phe Ala Phe Val Ser Glu Ala His Val Leu Ser 595 600 605	1824
AGC CTG GTC TAC TTC CAC TGC AGT GCC TTA ATC TGT AAT CGA CTC TCC Ser Leu Val Tyr Phe His Cys Ser Ala Leu Ile Cys Asn Arg Leu Ser 610 615 620	1872
CCT GAC TCC CCA CTG TGT TCT GTG ACC TGC CCT GTG TCC TCT AGG CAC Pro Asp Ser Pro Leu Cys Ser Val Thr Cys Pro Val Ser Ser Arg His 625 630 635 640	1920
AGG CGA GCC ACA GGG GCC ACT GAA GCA GAG AAA ATG ACA GTC AGC CTC Arg Arg Ala Thr Gly Ala Thr Glu Ala Glu Lys Met Thr Val Ser Leu 645 650 655	1968
CCA GGA CCC ATT CTC CTG TTG TCA GAT GAC TCC TCA TTC AGA GGT GTC Pro Gly Pro Ile Leu Leu Leu Ser Asp Ser Ser Phe Arg Gly Val 660 665 670	2016
GGC TCA TCT GAT CTA AAA GCA AGT GGG AGC AGT GGG GAG AAG ACT AGG Gly Ser Ser Asp Leu Lys Ala Ser Gly Ser Ser Gly Glu Lys Ser Arg 675 680 685	2064
AGT GAA ACA GGG GAG GAG GTT GGC TCA CGA GGT GCT ATG GAC ACC AAA Ser Glu Thr Gly Glu Glu Val Gly Ser Arg Gly Ala Met Asp Thr Lys 690 695 700	2112

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GGG CAC AAG ACT GCT GGA GAT GTT GGT TCC AAA GCT GTG GCT GCT GTG 2160
 Gly His Lys Thr Ala Gly Asp Val Gly Ser Lys Ala Val Ala Ala Val
 705 710 715 720

GCT GCC TTT GCA GGT GTG GTG GCA ACT CTA GGC TTC ATC TAC TAC CTG 2208
 Ala Ala Phe Ala Gly Val Val Ala Thr Leu Gly Phe Ile Tyr Tyr Leu
 725 730 735

TAC GAG AAA AGG ACT GTG TCA AAT CAC TAAATGGGCT TCTAAATAAA 2255
 Tyr Glu Lys Arg Thr Val Ser Asn His
 740 745

GCAGTCAAAA T 2266

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Ala Cys Arg Gln Arg Gly Gly Ser Trp Ser Pro Ser Gly Trp Phe
 1 5 10 15

Asn Ala Gly Trp Ser Thr Tyr Arg Ser Ile Ser Leu Phe Phe Ala Leu
 20 25 30

Val Thr Ser Gly Asn Ser Ile Asp Val Ser Gln Leu Val Asn Pro Ala
 35 40 45

Phe Pro Gly Thr Val Thr Cys Asp Glu Arg Glu Ile Thr Val Glu Phe
 50 55 60

Pro Ser Ser Pro Gly Thr Lys Lys Trp His Ala Ser Val Val Asp Pro
 65 70 75 80

Leu Gly Leu Asp Met Pro Asn Cys Thr Tyr Ile Leu Asp Pro Glu Lys
 85 90 95

Leu Thr Leu Arg Ala Thr Tyr Asp Asn Cys Thr Arg Arg Val His Gly
 100 105 110

Gly His Gln Met Thr Ile Arg Val Met Asn Asn Ser Ala Ala Leu Arg
 115 120 125

His Gly Ala Val Met Tyr Gln Phe Phe Cys Pro Ala Met Gln Val Glu
 130 135 140

Glu Thr Gln Gly Leu Ser Ala Ser Thr Ile Cys Gln Lys Asp Phe Met
 145 150 155 160

Ser Phe Ser Leu Pro Arg Val Phe Ser Gly Leu Ala Asp Asp Ser Lys
 165 170 175

Gly Thr Lys Val Gln Met Gly Trp Ser Ile Glu Val Gly Asp Gly Ala
 180 185 190

Arg Ala Lys Thr Leu Thr Leu Pro Glu Ala Met Lys Glu Gly Phe Ser
 195 200 205

Leu Leu Ile Asp Asn His Arg Met Thr Phe His Val Pro Phe Asn Ala
 210 215 220

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Thr Gly Val Thr His Tyr Val Gln Gly Asn Ser His Leu Tyr Met Val
 225 230 235 240
 Ser Leu Lys Leu Thr Phe Ile Ser Pro Gly Gln Lys Val Ile Phe Ser
 245 250 255
 Ser Gln Ala Ile Cys Ala Pro Asp Pro Val Thr Cys Asn Ala Thr His
 260 265 270
 Met Thr Leu Thr Ile Pro Glu Phe Pro Gly Lys Leu Lys Ser Val Ser
 275 280 285
 Phe Glu Asn Gln Asn Ile Asp Val Ser Gln Leu His Asp Asn Gly Ile
 290 295 300
 Asp Leu Glu Ala Thr Asn Gly Met Lys Leu His Phe Ser Lys Thr Leu
 305 310 315 320
 Leu Lys Thr Lys Leu Ser Glu Lys Cys Leu Leu His Gln Phe Tyr Leu
 325 330 335
 Ala Ser Leu Lys Leu Thr Phe Leu Leu Arg Pro Glu Thr Val Ser Met
 340 345 350
 Val Ile Tyr Pro Glu Cys Leu Cys Glu Ser Pro Val Ser Ile Val Thr
 355 360 365
 Gly Glu Leu Cys Thr Gln Asp Gly Phe Met Asp Val Glu Val Tyr Ser
 370 375 380
 Tyr Gln Thr Gln Pro Ala Leu Asp Leu Gly Thr Leu Arg Val Gly Asn
 385 390 395 400
 Ser Ser Cys Gln Pro Val Phe Glu Ala Gln Ser Gln Gly Leu Val Arg
 405 410 415
 Phe His Ile Pro Leu Asn Gly Cys Gly Thr Arg Tyr Lys Phe Glu Asp
 420 425 430
 Asp Lys Val Val Tyr Glu Asn Glu Ile His Ala Leu Trp Thr Asp Phe
 435 440 445
 Pro Pro Ser Lys Ile Ser Arg Asp Ser Glu Phe Arg Met Thr Val Lys
 450 455 460
 Cys Ser Tyr Ser Arg Asn Asp Met Leu Leu Asn Ile Asn Val Glu Ser
 465 470 475 480
 Leu Thr Pro Pro Val Ala Ser Val Lys Leu Gly Pro Phe Thr Leu Ile
 485 490 495
 Leu Gln Ser Tyr Pro Asp Asn Ser Tyr Gln Gln Pro Tyr Gly Glu Asn
 500 505 510
 Glu Tyr Pro Leu Val Arg Phe Leu Arg Gln Pro Ile Tyr Met Glu Val
 515 520 525
 Arg Val Leu Asn Arg Asp Asp Pro Asn Ile Lys Leu Val Leu Asp Asp
 530 535 540
 Cys Trp Ala Thr Ser Thr Met Asp Pro Asp Ser Phe Pro Gln Trp Asn
 545 550 555 560
 Val Val Val Asp Gly Cys Ala Tyr Asp Leu Asp Asn Tyr Gln Thr Thr
 565 570 575
 Phe His Pro Val Gly Ser Ser Val Thr His Pro Asp His Tyr Gln Arg

580

585

590

Phe Asp Met Lys Ala Phe Ala Phe Val Ser Glu Ala His Val Leu Ser
595 † 600 605

Ser Leu Val Tyr Phe His Cys Ser Ala Leu Ile Cys Asn Arg Leu Ser
610 615 620

Pro Asp Ser Pro Leu Cys Ser Val Thr Cys Pro Val Ser Ser Arg His
625 630 635 640

Arg Arg Ala Thr Gly Ala Thr Glu Ala Glu Lys Met Thr Val Ser Leu
645 650 655

Pro Gly Pro Ile Leu Leu Leu Ser Asp Asp Ser Ser Phe Arg Gly Val
660 665 670

Gly Ser Ser Asp Leu Lys Ala Ser Gly Ser Ser Gly Glu Lys Ser Arg
675 680 685

Ser Glu Thr Gly Glu Glu Val Gly Ser Arg Gly Ala Met Asp Thr Lys
690 695 700

Gly His Lys Thr Ala Gly Asp Val Gly Ser Lys Ala Val Ala Ala Val
705 710 715 720

Ala Ala Phe Ala Gly Val Val Ala Thr Leu Gly Phe Ile Tyr Tyr Leu
725 730 735

Tyr Glu Lys Arg Thr Val Ser Asn His
740 745

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 15..506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAATTGCGG CCGC TCC TGT GTG ACC CAT CCT GAT CAC TAT CAG AGG TTT 50
Ser Ser Val Thr His Pro Asp His Tyr Gln Arg Phe
1 5 10

GAC ATG AAG GCT TTT GCC TTT GTA TCA GAG GCC CAT GTG CTC TCT AGC 98
Asp Met Lys Ala Phe Ala Phe Val Ser Glu Ala His Val Leu Ser Ser
15 20 25

CTG GTC TAC TTC CAC TGC AGT GCC TTA ATC TGC AAT CGA CTC TCT CCA 146
Leu Val Tyr Phe His Cys Ser Ala Leu Ile Cys Asn Arg Leu Ser Pro
30 35 40

GAC TCC CCT CTG TGT TCT GTG ACC TGC CCT GTG TCA TCT AGG CAC AGG 194
Asp Ser Pro Leu Cys Ser Val Thr Cys Pro Val Ser Ser Arg His Arg
45 50 55 60

CGA GCC ACA GGG GCC ACT GAA GCA GAG AAA ATG ACA GTC AGC CTC CCA 242

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Arg Ala Thr Gly Ala Thr Glu Ala Glu Lys Met Thr Val Ser Leu Pro
65 70 75

GGA CCC ATT CTC CTG TTT TCA GAC GAC TCC TCA TTC AGA GGT GTT GGC 290
Gly Pro Ile Leu Leu Ser Asp Asp Ser Ser Phe Arg Gly Val Gly
80 85 90

TCA TCT GAT CTA AAA GCA AGT GGG AGC AGT GGG GAG AAC AGT AGG AGC 338
Ser Ser Asp Leu Lys Ala Ser Gly Ser Ser Gly Glu Asn Ser Arg Ser
95 100 105

GAA ACA GGG GAG GAG GTT GGC TCA CGA GAT GTT ATG GAC ACC AAA GGG 386
Glu Thr Gly Glu Glu Val Gly Ser Arg Asp Val Met Asp Thr Lys Gly
110 115 120

CAC AGG ACT GCT GGA GAT GTT GGT TCC AAA GCT GTG GCT GCT GTG GCT 434
His Arg Thr Ala Gly Asp Val Gly Ser Lys Ala Val Ala Ala Val Ala
125 130 135 140

GCC TTG GCA GGT GTG GTG GCA ACT CTA GGC TTC ATC TGT TAC CTG TAT 482
Ala Leu Ala Gly Val Val Ala Thr Leu Gly Phe Ile Cys Tyr Leu Tyr
145 150 155

AAG AAA AGG ACT GTG TCA AAT CAC TAAATGGGCT TCTAAATAAA GCAGTCAAAA 536
Lys Lys Arg Thr Val Ser Asn His
160

TAAAAAAGAA GCGGCCGCGA ATTC 560

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Ser Val Thr His Pro Asp His Tyr Gln Arg Phe Asp Met Lys Ala
1 5 10 15

Phe Ala Phe Val Ser Glu Ala His Val Leu Ser Ser Leu Val Tyr Phe
20 25 30

His Cys Ser Ala Leu Ile Cys Asn Arg Leu Ser Pro Asp Ser Pro Leu
35 40 45

Cys Ser Val Thr Cys Pro Val Ser Ser Arg His Arg Arg Ala Thr Gly
50 55 60

Ala Thr Glu Ala Glu Lys Met Thr Val Ser Leu Pro Gly Pro Ile Leu
65 70 75 80

Leu Leu Ser Asp Asp Ser Ser Phe Arg Gly Val Gly Ser Ser Asp Leu
85 90 95

Lys Ala Ser Gly Ser Ser Gly Glu Asn Ser Arg Ser Glu Thr Gly Glu
100 105 110

Glu Val Gly Ser Arg Asp Val Met Asp Thr Lys Gly His Arg Thr Ala
115 120 125

Gly Asp Val Gly Ser Lys Ala Val Ala Ala Val Ala Ala Leu Ala Gly
130 135 140

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Val Val Ala Thr Leu Gly Phe Ile Cys Tyr Leu Tyr Lys Lys Arg Thr
 145 150 155 160

Val Ser Asn His

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 866 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 12..821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTCGCGG C CGC CGT GGC TCT GTC ACT CGT GAC AGC ATC TTC AGG CTC	50
Arg Arg Gly Ser Val Thr Arg Asp Ser Ile Phe Arg Leu	
1 5 10	
CAT GTC AGC TGC AGC TAC TCA GTA AGT AGC AAC TCT CTC CCA ATC AAG	98
His Val Ser Cys Ser Tyr Ser Val Ser Ser Asn Ser Leu Pro Ile Lys	
15 20 25	
GTC CAG GTT TTT ACT CTC CCA CCA CCC TTT CCT GAG ACC CAG CCT GGA	146
Val Gln Val Phe Thr Leu Pro Pro Pro Phe Pro Glu Thr Gln Pro Gly	
30 35 40 45	
CCC CTC ACT CTG GAA CTT CAG ATT GCC AAA GAT AAA AAC TAT GGC TCC	194
Pro Leu Thr Leu Glu Leu Gln Ile Ala Lys Asp Lys Asn Tyr Gly Ser	
50 55 60	
TAC TAT GGT GTT GGT GAC TAC CCC GTG GTG AAG TTG CTT CGG GAT CCC	242
Tyr Tyr Gly Val Gly Asp Tyr Pro Val Val Lys Leu Leu Arg Asp Pro	
65 70 75	
ATC TAT GTG GAG GTC TCC ATC CTT CAC AGA ACA GAC CCC TCC CTG GGG	290
Ile Tyr Val Glu Val Ser Ile Leu His Arg Thr Asp Pro Ser Leu Gly	
80 85 90	
CTG CTC CTA CAT CAG TGT TGG GCA ACA CCC AGC ACA GAC CCA CTG AGT	338
Leu Leu Leu His Gln Cys Trp Ala Thr Pro Ser Thr Asp Pro Leu Ser	
95 100 105	
CAG CCA CAG TGG CCC ATC CTG GTA AAG GGC TGC CCC TAC ATT GGA GAC	386
Gln Pro Gln Trp Pro Ile Leu Val Lys Gly Cys Pro Tyr Ile Gly Asp	
110 115 120 125	
AAC TAT CAG ACC CAG CTG ATC CCT GTC CAG AAA GCC TTG GAT CTT CCA	434
Asn Tyr Gln Thr Gln Leu Ile Pro Val Gln Lys Ala Leu Asp Leu Pro	
130 135 140	
TTT CCC TCT CAC TAC CAG CGC TTC AGC ATC TTC ACC TTC AGC TTT GTG	482
Phe Pro Ser His Tyr Gln Arg Phe Ser Ile Phe Thr Phe Ser Phe Val	
145 150 155	
GAC CCT ACA GCG GAG AAA CAG GCC CTC AGG GGA CCG GTG CAT CTG CAC	530
Asp Pro Thr Ala Glu Lys Gln Ala Leu Arg Gly Pro Val His Leu His	
160 165 170	

- 131 -

TGC AGT GTG TCA GTC TGC CAG CCT GCT GAG ACA CCA TCC TGT GCG GTA	578
Cys Ser Val Ser Val Cys Gln Pro Ala Glu Thr Pro Ser Cys Ala Val	
175 180 185	
ACC TGT CCT GAT CTC AGT CGA AGA AAT TCA GGC ACC ATT TTT CAG AAC	626
Thr Cys Pro Asp Leu Ser Arg Arg Asn Ser Gly Thr Ile Phe Gln Asn	
190 195 200 205	
ACT ACT GCT AGT GTT TCT AGC AAA GGC CCC ATG ATT CTA CTC CAA GCC	674
Thr Thr Ala Ser Val Ser Ser Lys Gly Pro Met Ile Leu Leu Gln Ala	
210 215 220	
ACT AAG GAC CCT CCA GAA AAG CTC CGT GCT CCT GTA GAC TCA AAA GTT	722
Thr Lys Asp Pro Pro Glu Lys Leu Arg Ala Pro Val Asp Ser Lys Val	
225 230 235	
CTG TGG GTG GCA GGC CTT TCT GGG ACC TTA ATC CTT GGA GGC TTA GTA	770
Leu Trp Val Ala Gly Leu Ser Gly Thr Leu Ile Leu Gly Gly Leu Val	
240 245 250	
GTA TCC TAC TTG GCT ATC AAA CAG CTG AAT TGT CCA GAC CAA ACA TGT	818
Val Ser Tyr Leu Ala Ile Lys Gln Leu Asn Cys Pro Asp Gln Thr Cys	
255 260 265	
CAA TAAACCAGA CTGTACTCCC AAAAAAAAAA AGCGGCCGCG AATTC	866
Gln	
270	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Arg Arg Gly Ser Val Thr Arg Asp Ser Ile Phe Arg Leu His Val Ser	
1 5 10 15	
Cys Ser Tyr Ser Val Ser Ser Asn Ser Leu Pro Ile Lys Val Gln Val	
20 25 30	
Phe Thr Leu Pro Pro Pro Phe Pro Glu Thr Gln Pro Gly Pro Leu Thr	
35 40 45	
Leu Glu Leu Gln Ile Ala Lys Asp Lys Asn Tyr Gly Ser Tyr Tyr Gly	
50 55 60	
Val Gly Asp Tyr Pro Val Val Lys Leu Leu Arg Asp Pro Ile Tyr Val	
65 70 75 80	
Glu Val Ser Ile Leu His Arg Thr Asp Pro Ser Leu Gly Leu Leu Leu	
85 90 95	
His Gln Cys Trp Ala Thr Pro Ser Thr Asp Pro Leu Ser Gln Pro Gln	
100 105 110	
Trp Pro Ile Leu Val Lys Gly Cys Pro Tyr Ile Gly Asp Asn Tyr Gln	
115 120 125	
Thr Gln Leu Ile Pro Val Gln Lys Ala Leu Asp Leu Pro Phe Pro Ser	
130 135 140	

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His Tyr Gln Arg Phe Ser Ile Phe Thr Phe Ser Phe Val Asp Pro Thr
145                      150                      155                      160

Ala Glu Lys Gln Ala Leu Arg Gly Pro Val His Leu His Cys Ser Val
                      165                      170                      175

Ser Val Cys Gln Pro Ala Glu Thr Pro Ser Cys Ala Val Thr Cys Pro
                      180                      185                      190

Asp Leu Ser Arg Arg Asn Ser Gly Thr Ile Phe Gln Asn Thr Thr Ala
                      195                      200                      205

Ser Val Ser Ser Lys Gly Pro Met Ile Leu Leu Gln Ala Thr Lys Asp
                      210                      215                      220

Pro Pro Glu Lys Leu Arg Ala Pro Val Asp Ser Lys Val Leu Trp Val
225                      230                      235                      240

Ala Gly Leu Ser Gly Thr Leu Ile Leu Gly Gly Leu Val Val Ser Tyr
                      245                      250                      255

Leu Ala Ile Lys Gln Leu Asn Cys Pro Asp Gln Thr Cys Gln
                      260                      265                      270

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(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 722 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 15..683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GAATTCGCGG CCGC ATC CAC ACT GGC AGC CAC GTG CCA CTG CGG TTG TTT      50
      Ile His Thr Gly Ser His Val Pro Leu Arg Leu Phe
          1                      5                      10

GTG GAC CAC TGC GTG GCC ACA CCA ACA CCA GAC CAG AAT GCC TCC CCT      98
Val Asp His Cys Val Ala Thr Pro Thr Pro Asp Gln Asn Ala Ser Pro
      15                      20                      25

TAT CAC ACC ATC GTG GAC TTC CAT GGC TGT CTT GTC GAT GGT CTC ACT     146
Tyr His Thr Ile Val Asp Phe His Gly Cys Leu Val Asp Gly Leu Thr
      30                      35                      40

GAT GCC TCT TCT GCG TTC AAA GTT CCT CGA CCC GGG CCA GAT ACA CTC     194
Asp Ala Ser Ser Ala Phe Lys Val Pro Arg Pro Gly Pro Asp Thr Leu
      45                      50                      55                      60

CAG TTC ACA GTG GAT GTC TTC CAC TTT GCT AAT GAC TCC AGA AAC ATG     242
Gln Phe Thr Val Asp Val Phe His Phe Ala Asn Asp Ser Arg Asn Met
          65                      70                      75

ATA TAC ATC ACC TGC CAC CTG AAG GCC ATC CCA GCT GAG CAG GAA CCA     290
Ile Tyr Ile Thr Cys His Leu Lys Ala Ile Pro Ala Glu Gln Glu Pro
          80                      85                      90

GAC GAA CTC AAC AAA GCC TGT TCC TTC AGC AAG TCT TCC AAC AGC TGG     338

```


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(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ile	His	Thr	Gly	Ser	His	Val	Pro	Leu	Arg	Leu	Phe	Val	Asp	His	Cys
1				5					10					15	
Val	Ala	Thr	Pro	Thr	Pro	Asp	Gln	Asn	Ala	Ser	Pro	Tyr	His	Thr	Ile
			20					25					30		
Val	Asp	Phe	His	Gly	Cys	Leu	Val	Asp	Gly	Leu	Thr	Asp	Ala	Ser	Ser
		35					40					45			
Ala	Phe	Lys	Val	Pro	Arg	Pro	Gly	Pro	Asp	Thr	Leu	Gln	Phe	Thr	Val
	50					55					60				
Asp	Val	Phe	His	Phe	Ala	Asn	Asp	Ser	Arg	Asn	Met	Ile	Tyr	Ile	Thr
65				70						75					80
Cys	His	Leu	Lys	Ala	Ile	Pro	Ala	Glu	Gln	Glu	Pro	Asp	Glu	Leu	Asn
				85					90					95	
Lys	Ala	Cys	Ser	Phe	Ser	Lys	Ser	Ser	Asn	Ser	Trp	Phe	Pro	Val	Glu
			100					105					110		

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Gly Pro Ala Asp Ile Cys Gln Cys Cys Ser Lys Gly Asp Cys Gly Thr
 115 120 125
 Pro Ser His Ser Arg Arg Gln Pro His Val Val Ser Gln Trp Ser Arg
 130 135 140
 Ser Ala Ser Arg Asn Arg Arg His Val Thr Glu Glu Ala Asp Ile Thr
 145 150 155 160
 Val Gly Pro Leu Ile Phe Leu Asp Arg Ser Ala Asp Tyr Glu Val Glu
 165 170 175
 Gln Trp Ala Leu Pro Thr Asp Thr Ser Val Leu Leu Leu Gly Ile Gly
 180 185 190
 Leu Ala Val Val Ala Ser Leu Thr Leu Thr Ala Val Ile Leu Ile Phe
 195 200 205
 Thr Arg Arg Trp Arg Thr Ala Ser Arg Pro Val Ser Val Ser Gln
 210 215 220

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCCCTTCCC AGCAACTGCA CCATCACCAC CATGGG

36

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCCCCATG GTGGTGGTGA TGGTGCA GTT GCTGGGAAGG GCGAT

45

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCCCTCGA GCCACCATCA CCACCATCAT G

31

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AATTCATGAT GGTGGTGATG GTGGCTCGAG G

31

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCCGGATCCG CAGACCATCT GGCCAACTGA G

31

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCGCTCGAGG GCATATGGCT GCCAGTGTG

29

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCGCTAGCA GATCTATGGC GCGAGCTGG AGGTTT

36

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGCGGATCCT ATTAATGGTG GTGATGGTGG TGACTAGTGG ACCCTTCCA

49

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCCGCTAGCA GATCTATGGG GCTGAGCTAT GGAATTTTC

39

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

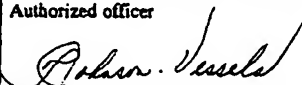
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CGCACTAGTT GACCCCTCTA TACCATGATC ACTA

34

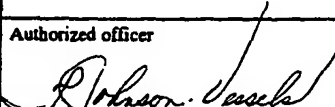
INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 37 line 28 and page 38, lines 1-3	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit January 27, 1993	Accession Numbers 75406 and 75405
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<p>"In respect of those designations in which a European patent is sought, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 23(4) EPC)."</p>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
<div>For receiving Office use only</div> <div><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div>Authorized officer </div>	<div>For International Bureau use only</div> <div><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div>Authorized officer</div>

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>39</u> , lines <u>13-16</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit January 27, 1993	Accession Numbers 75404 and 75403
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<p>"In respect of those designations in which a European patent is sought, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 23(4) EPC)."</p>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit") 	
For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application Authorized officer 	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer

WE CLAIM:

1. A method for inducing reproducible transient infertility in a mammal which comprises administering to a subject mammal a dose of a zona pellucida protein or fragment thereof, said proteins being selected from the group consisting of mammalian ZPA, mammalian ZPB, and combinations thereof, effective to stimulate production in said mammal of antibodies which recognize ZPA or ZPB protein of said mammal.
5
2. The method of claim 1, wherein said mammalian ZPA and ZPB are derived from the same mammalian species as the subject mammal.
10
3. The method of claim 1 wherein said mammalian ZPA and ZPB are derived from a mammalian species other than the subject mammal.
4. The method of claim 1, wherein said mammalian ZPA or ZPB protein is selected from the group consisting of porcine, canine, feline, bovine, cynomolgus monkey, and human ZPA and ZPB.
15
5. The method of claim 1 wherein said mammalian ZPA and mammalian ZPB are essentially devoid of ZPC.
6. The method of claim 1 wherein said zona pellucida protein is substantially only ZPA.
20
7. The method of claim 1 wherein said zona pellucida protein is substantially only ZPB.

8. The method of claim 1 wherein said mammalian ZPA and ZPB is recombinant ZPA and ZPB.

9. The method of claim 1 wherein said antibodies have a titer of at least 1:250.

5 10. A method for inducing permanent sterility in a mammal which comprises administering to a subject mammal a dose of a recombinant mammalian ZPC protein or fragment thereof, effective to stimulate production in said mammal of antibodies which recognize the ZPC protein of said mammal.

10 11. The method of claim 10, wherein said mammalian ZPC protein is derived from the same species as the subject mammal.

12. The method of claim 10 wherein said ZPC is derived from a mammalian species other than the subject mammal.

15 13. The method of claim 10, wherein said mammalian ZPC protein is selected from the group consisting of porcine, rabbit, canine, feline, cynomolgus monkey, and bovine ZPC.

14. The method of claim 10 wherein said ZPC protein is essentially devoid of ZPA and ZPB.

20 15. A pharmaceutical composition comprising, an effective contraceptive dose of a recombinant ZPC protein or an immunocontraceptively active fragment thereof.

16. A pharmaceutical composition comprising an effective contraceptive dose of a zona pellucida protein selected from the group consisting of mammalian ZPA and ZPB, and fragments thereof, and pharmaceutically acceptable carriers, diluents and adjuvants.

5 17. The pharmaceutical composition of claim 16 wherein said mammalian ZPA and ZPB are derived from the same mammalian species as the subject mammal.

18. The pharmaceutical composition of claim 16, wherein said mammalian ZPA and ZPB are selected from the group consisting of
10 porcine, feline, canine, bovine, cynomolgus monkey, and human ZPA and ZPB.

19. The pharmaceutical composition of claim 16 wherein said mammalian ZPA and ZPB are essentially devoid of ZPC.

20. The pharmaceutical composition of claim 16, wherein said
15 mammalian ZPA and ZPB is recombinant ZPA and ZPB.

21. A purified and isolated DNA sequence encoding porcine ZPA, ZPB, ZPC, or immunocontraceptively active fragments thereof, said DNA sequences being essentially as set out in SEQ ID NOS. 1, 3, and 5.

22. A purified and isolated DNA sequence encoding rabbit
20 ZPC or an immunocontraceptively active fragment thereof, said DNA sequences being essentially as set out in SEQ ID NO. 7.

23. A purified and isolated DNA sequence encoding canine ZPA or ZPC, or immunocontraceptively active fragments thereof, said DNA sequences being essentially as set out in SEQ ID NOS. 9 and 11.

24. A purified and isolated DNA sequence encoding feline
5 ZPA, ZPB, or ZPC, or immunocontraceptively active fragments thereof, said DNA sequences being essentially as set out in SEQ ID NOS. 13, 15, and 17.

25. A purified and isolated DNA sequence encoding bovine ZPA, ZPB, or ZPC, or immunocontraceptively active fragments thereof, said DNA sequences being essentially as set out in SEQ ID NOS. 19, 21, and 23.

10 26. A purified and isolated DNA encoding human ZPA or immunocontraceptively active fragments thereof, comprising DNA present in the human DNA inserts in lambda phage clones A1 (ATCC No. 75404) and A4 (ATCC No. 75403).

15 27. A purified and isolated DNA encoding human ZPA or an immunocontraceptively active fragment thereof, said sequence being essentially as set out as SEQ ID NO. 42.

28. A purified isolated DNA encoding human ZPB or immunocontraceptively active fragments thereof, comprising human DNA present in the DNA inserts in lambda phage clones 1-1 (ATCC No. 75406)
20 and 4-9 (ATCC No. 75405).

29. A purified and isolated DNA encoding human ZPB or an immunocontraceptively active fragments thereof, said sequence being essentially as set out in SEQ ID NO. 40.

30. A vector containing the DNA sequence of claim 21.
31. A vector containing the DNA sequence of claim 22.
32. A vector containing the DNA sequence of claim 23.
33. A vector containing the DNA sequence of claim 24.
- 5 34. A vector containing the DNA sequence of claim 25.
35. A vector containing the DNA sequence claim 26.
36. A vector containing the DNA sequence of claim 27.
37. A vector containing the DNA sequence of claim 28.
38. A vector containing the DNA sequence of claim 29.
- 10 39. A procaryotic or eucaryotic host cell stably transformed or transfected with a vector according to claims 30, 31, 32, 33, 34, 35, 36, 37, or 38.
40. A polypeptide product of the expression in a procaryotic or eucaryotic host cell of a DNA sequence according to claims 21, 22, 23, 24, 15 25, 26, 27, 28 or 29.
41. A process for the production of a recombinant mammalian zona pellucida protein or fragment thereof, said process comprising:

growing, under suitable nutrient conditions, procaryotic or eucaryotic host cells transformed or transfected with a DNA vector according to claims 30, 31, 32, 33, 34, 35, 36, or 37 and isolating desired polypeptide products of the expression of DNA sequences in said vector.

5 42. A method for inducing reproducible transient infertility in a mammal, the method comprising, administering to a subject mammal a contraceptively effective dose of an antibody directed to a zona pellucida protein, said antibody selected from the group consisting of anti-ZPA antibodies and anti-ZPB antibodies.

10 43. A method for inducing permanent sterility in a mammal, the method comprising administering to a subject mammal a contraceptively effective dose of an antibody directed to ZPC.

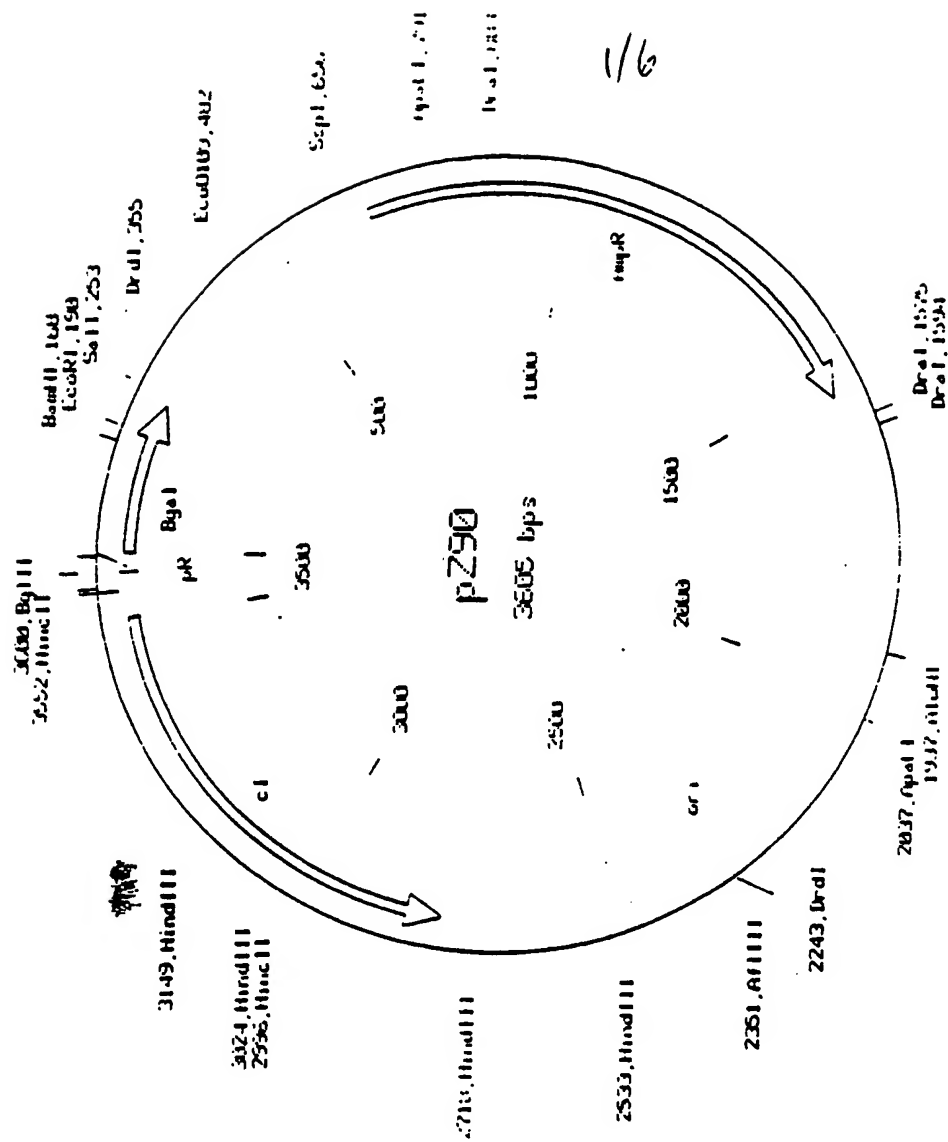


FIGURE 1

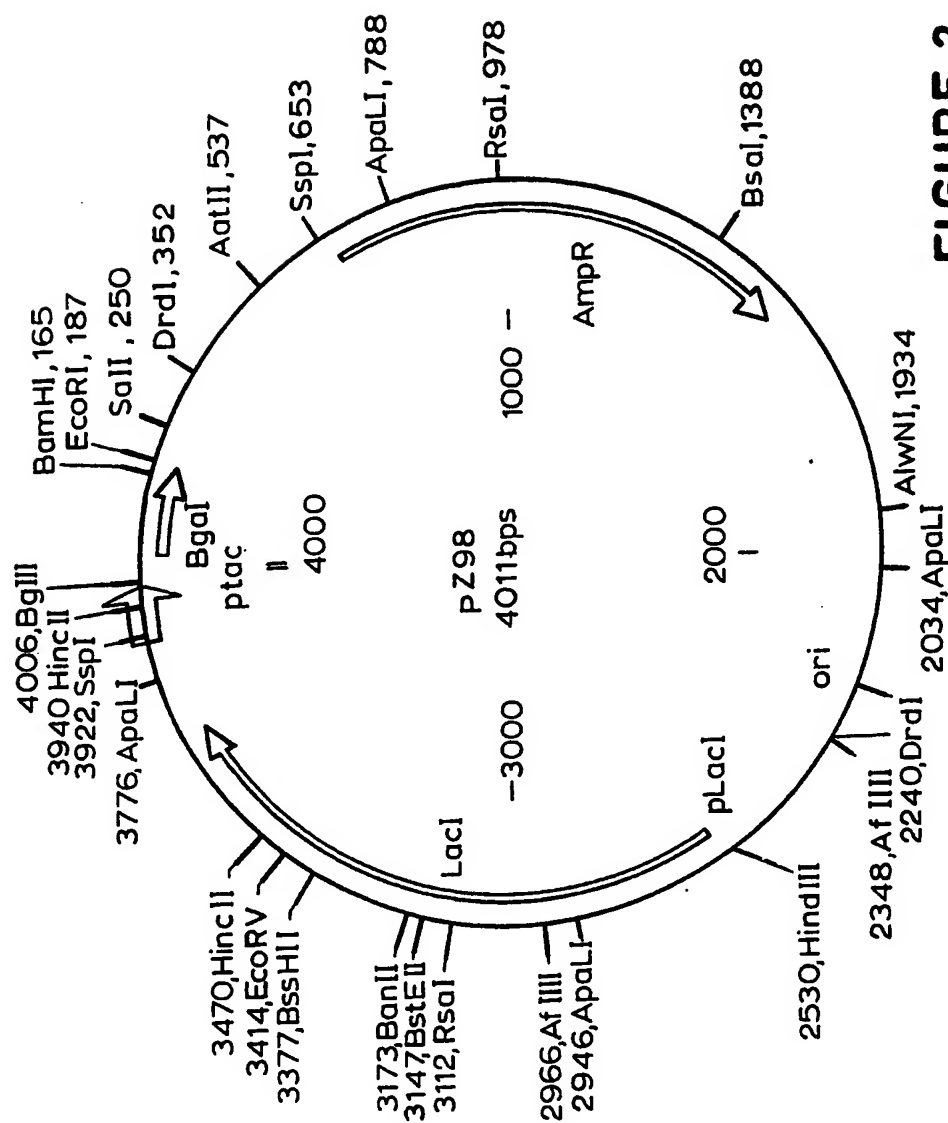


FIGURE 2

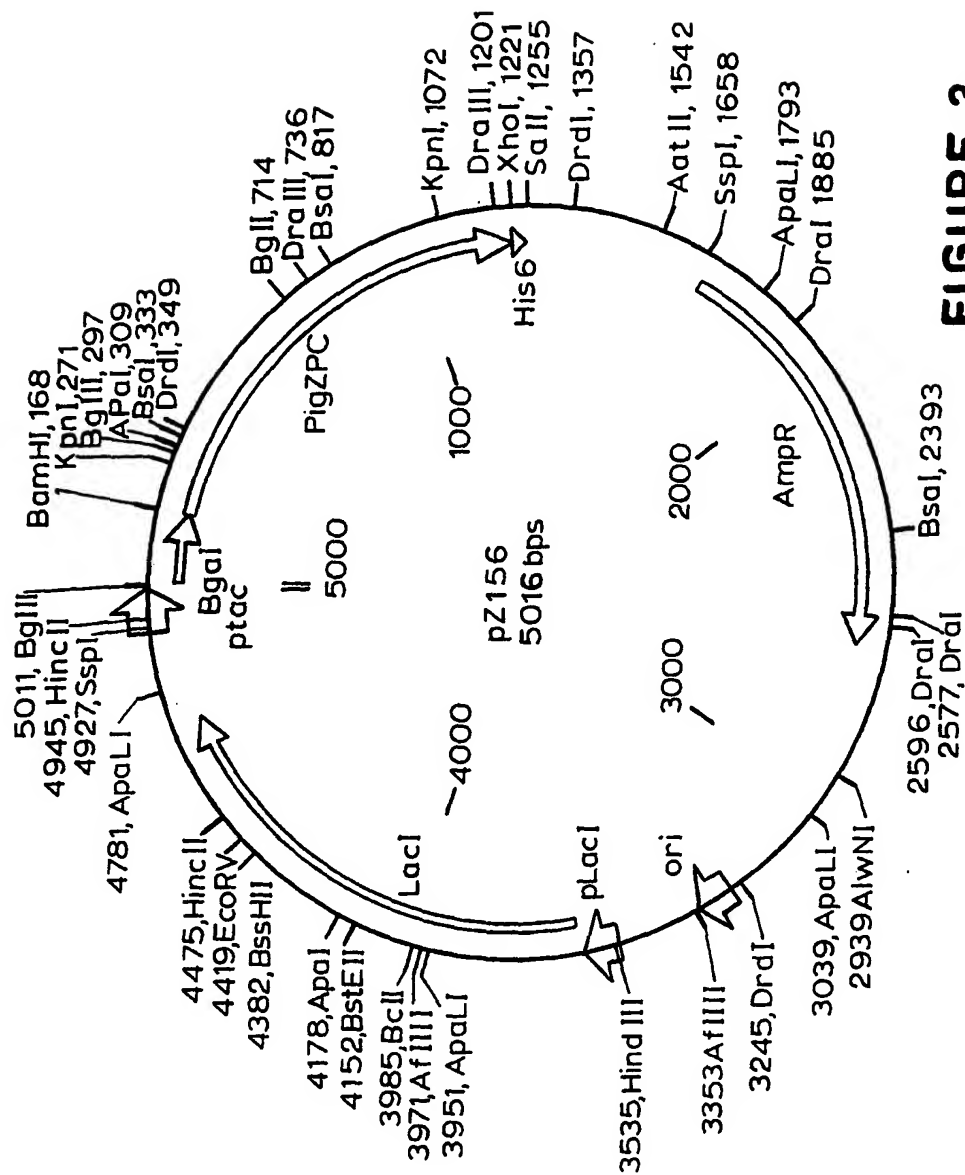
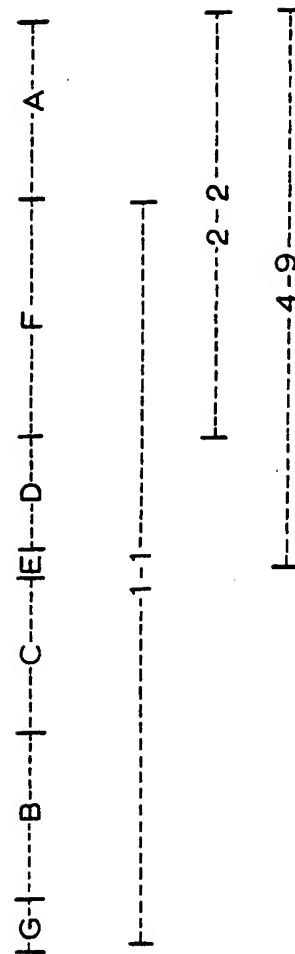
**FIGURE 3**

FIGURE. 4



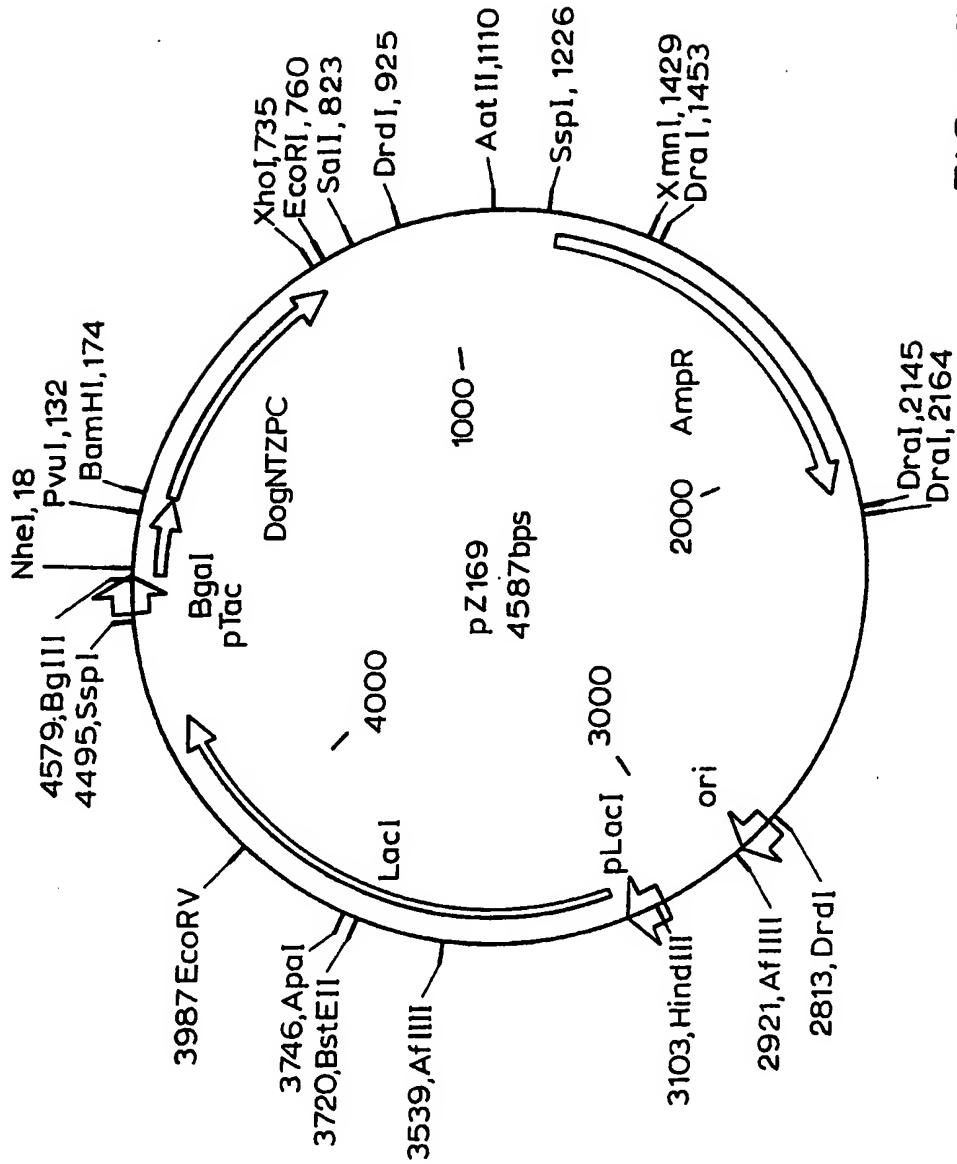


FIGURE 5

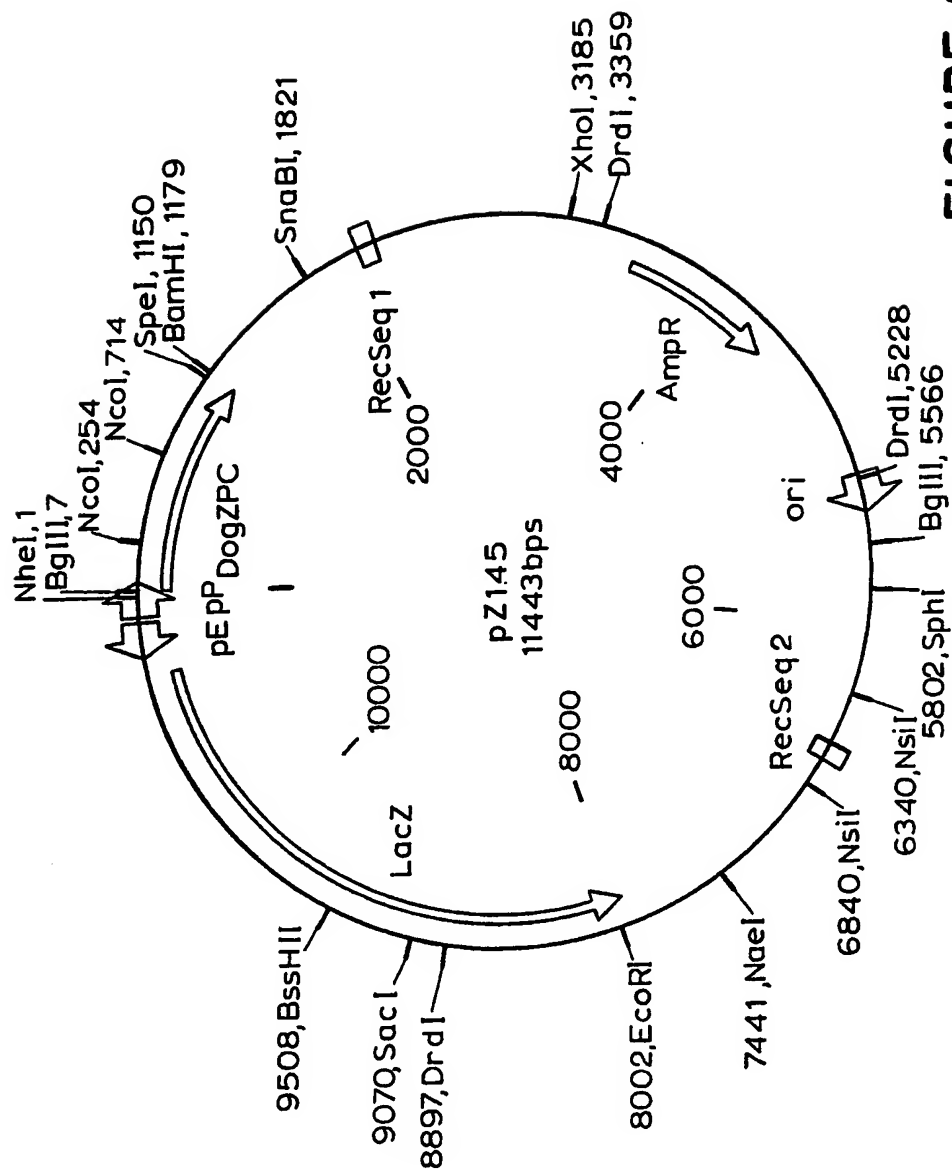


FIGURE 6

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US93/10851

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) : A61K 37/02, 39/00, 39/395; C07K 13/00; C12N 5/10, 15/12; C12P 21/00

US CL : 424/85.8, 88; 435/69.1, 69.3, 320.1; 536/23.1, 23.5

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/85.8, 88; 435/69.1, 69.3, 320.1; 536/23.1, 23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG, BIOSIS, EMBASE, MEDLINE, WPI

search terms: harris, zona pellucida, ZP3, ZPA, ZPB, ZPC, contraception

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US, A, 4,996,297 (Dunbar) 26 February 1991, see entire document.	1-43
Y	WO 90/15624 (Dean) 27 December 1990, see entire document.	1-43
Y	WO 92/03548 (Van Duin) 05 March 1992, see entire document.	1-43
Y	Proc. Natl. Acad. Sci., Volume 87, issued August 1990, M.E. Chamberlin et al., "Human Homolog of the Mouse Sperm Receptor", pages 6014-6018, see entire document.	1-43

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

Special categories of cited documents:	
A document defining the general state of the art which is not considered to be part of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
B earlier document published on or after the international filing date	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
O document referring to an oral disclosure, use, exhibition or other means	*A* document member of the same patent family
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

31 January 1994

Date of mailing of the international search report

MAR 11 1994

 Name and mailing address of the ISA/US
 Commissioner of Patents and Trademarks
 Box PCT
 Washington, D.C. 20231

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Authorized officer

PHILLIP GAMBEL

Telephone No. (703) 305-0196

Phillip Warden for

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/10851

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Developmental Biology, Volume 127, issued October 1988, M.J. Ringuette et al., "Molecular Analysis of cDNA Coding for ZP3, a Sperm Binding Protein of the Mouse Zona Pellucida", page 287-295, see entire document.	1-43
Y	Biology of Reproduction, Volume 44, issued April 1992, J.A. Keenan et al., "Endocrine Response in Rabbits Immunized with Native Versus Deglycosylated Porcine Zona Pellucida Antigens, page 150-156, see entire document.	1-43
Y	Biology of Reproduction, Volume 41, issued December 1989, A.G. Sacco et al., "Porcine Zona Pellucida: Association of Sperm Receptor Activity with the alpha-Glycoprotein Component of the Mr=55,000 Family", pages 523-532, see entire document.	1-43
Y	J. Biol. Chem., Volume 262, issued 15 January 1987, E.C. Yurewicz et al., "Structural Characterization of the Mr=55,000 Antigen (ZP3) of Porcine Oocyte Zona Pellucida", pages 564-571, see entire document.	1-43

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/10851

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

- I. Claims 1-9, 16-20, 40 and 42 drawn to a method of inducing transient infertility and pharmaceutical compositions comprising ZPA or ZPB proteins, classified in Class 424, subclass 88 and 85.8.
- II. Claims 10-15, 40 and 43 drawn to a method of inducing permanent sterility and pharmaceutical compositions with ZPC proteins, classified in Class 424, subclass 88 and 85.8.
- III. Claims 21-39 and 41, drawn to DNA and expression vectors for zona pellucida proteins and a process of producing recombinant proteins, classified in Class 435, subclasses 69.1 and 69.3, 320.1 and Class 536, subclasses 22.1 and 23.5.

The inventions listed as Groups I/II/III do not meet the requirements for Unity of Invention for the following reasons:

Group I is drawn to a first product and a first method of use, Group II is drawn to second product and a second method of use; and Group III is drawn to a third product. PCT Rule 13 does not provide for multiple products or methods within a single application. These inventions require different ingredients and process steps to accomplish the use of ZPA-, ZPB-, ZPC-specific proteins and ZPA-, ZPB-, ZPC-specific antibodies. Proteins (pharmaceutical compositions) and DNA (and its vectors) are distinct because their structures and modes of action are different. Furthermore, this application contains claims directed to the following patentably distinct species of the claimed inventions I, II and III: wherein the zona pellucida protein specificity is (a) ZPA, (b) ZPB or (c) ZPC. These species are distinct because their structures and modes of action are different; the substitution of one for another would not lead to the same effects.